

IMBA Expert™ OCAS/ORAU-Edition (Vers. 4.0)

User Manual

Appendix D: Example Bioassay Cases

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This Appendix provides worked examples of bioassay calculations performed by **IMBA Expert™ OCAS/ORAU-Edition**. The examples will introduce you to the main "built-in" features and functions that are provided for bioassay analysis, *i.e.*, for the assessment of intake(s) of radionuclides based on bioassay measurements.

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D.1. Introduction

The following case examples (taken from real cases) illustrate the main features provided in [IMBA Expert™ OCAS/ORAU-Edition](#) for estimating intake(s) from bioassay data:

- Calculation of a single intake.
- Calculation of multiple intakes.
- Calculation using multiple bioassay data sets.
- Uranium isotopic mixtures.
- Routine tritium urinalysis.
- Am-241 lung counting (for Pu-241).
- Calculations using Least Squares fitting.
- Calculations using Bayesian analysis.
- Transdermal uptake of I-125 from a wound.

D.2. Estimating a Single Intake

This example is one of the study cases taken from *IAEA (1999)* - see their Annex IV Case 3. The data are whole-body activity measurements of ^{60}Co commencing 1 day after an accidental inhalation of a cobalt metal and/or oxide aerosol. All external body surface contamination was removed by shower-bathing. A profile scan indicated dominant lung deposition. The accident occurred on February 24th, 1988. The whole-body activity measurements are given in Table D.1.

Table D.1. ^{60}Co whole-body measurement results.

Measurement date	Whole-body activity (Bq)
February 25, 1988	2720
March 1, 1988	1150
March 11, 1988	1010
March 28, 1988	790
May 16, 1988	482
August 11, 1988	358
November 29, 1990	78
February 19, 1992	35

The following steps (in the listed order) are recommended for calculating the amount of a **single intake (by inhalation)** from a set of **whole-body measurements** - where the time of the intake is known, and the aerosol and absorption parameters of the inhaled material can be specified with reasonable confidence. The additional steps required for a more complicated assessment

(involving *multiple intakes with unknown parameters*) are described in Section D.3.

1. Select the Indicator Nuclide - in the **Main Screen**.
2. Define the Reference Date - in the **Main Screen**.
3. Select the Reference Activity Units - in the **Main Screen**.
4. Select the **Bioassay Model** and other required Model Parameters - in the **Main Screen**.
5. Define the Intake Regime (IR1) - in the **Main Screen**.
6. Select - in the **Bioassay Calculations** screen - the **Bioassay Quantity** as "Whole body" (for display in the top **Bioassay Quantity** window).
7. Enter the bioassay data - using the data entry "tool" in the **Bioassay Quantity** window.
8. Graph the bioassay data - using the graph set up "tool" in the **Bioassay Quantity** window.
9. Select which bioassay data to use ("Whole body") and click "Start Calculation."
10. Improve the **data fit** using the Graph of the **Bioassay Quantity**.

D.2.1. Indicator Nuclide for Single Intake

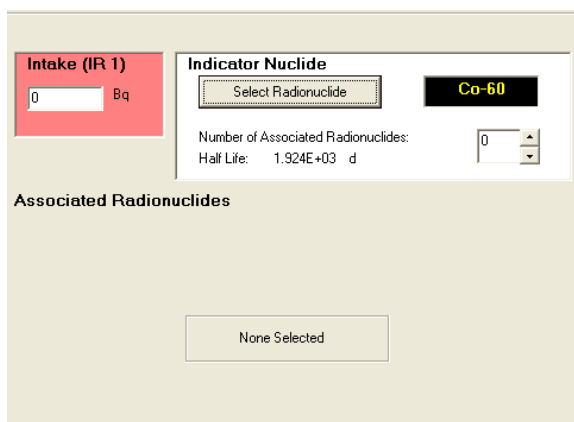


Figure D.1. Selecting the Indicator Nuclide (^{60}Co).

Select the **Indicator Nuclide** (^{60}Co in this example case) from the top-right-corner of the **Main Screen** (Figure D.1). **IMBA Expert™ OCAS/ORAU-Edition** will then be able to select automatically the **bioassay model(s)** appropriate for cobalt, and automatically take into account the **radioactive half-life** of ^{60}Co .



Tip: In this example case, we are using bioassay data to **calculate the intake**. Therefore, it is NOT necessary to enter a (hypothetical) value in the displayed "Intake (IR 1)" dialog box. **IMBA Expert™ OCAS/ORAU-Edition** will automatically display the **calculated** value of **Intake** in the dialog boxes in both the **Main Screen** and **Bioassay Calculations** screen.

D.2.2. Reference Date for Single Intake

IMBA Expert™ OCAS/ORAU-Edition keeps track of the **Intake** and all **bioassay measurements** on a common timescale. All events are timed with respect to a single **Reference Date** (and time-of-day, if necessary). The **Reference Date** is defined in the **Main Screen** (Figure D.2). The **IMBA System** must always have a reference date - even if you are working entirely in the **Time (d)** mode. The **default** value (January 1st, 1980) is loaded at start-up.

The 'Intake Scenario' dialog box is shown. On the left, under 'Intake Regimes', there is a 'Clear All Intake Regimes' button and a field 'Enter Number of Intake Regimes (1-10)' with a value of 1. Below this is a tabbed interface with 'IR 1' selected. Inside the 'IR 1' tab, there are two sections: 'Route' with radio buttons for Inhalation, Ingestion, Injection, Wound, and Vapor; and 'Mode' with radio buttons for Acute and Chronic. A 'Start Time (d)' field is set to 0. An 'Edit Complex Regime' button is at the bottom. On the right, the 'Units' section has 'Specify Time As' with 'Date' selected and 'Time (d) since' with a date field set to 1/1/1980. Below this are 'Intake' units (Bq, dpm, pCi, mg) and 'Dose' units (Sv, rem, mSv, mrem). A red box labeled 'Intake (IR 1)' shows a value of 0 Bq. To the right of the units is an 'Associated Radionuclide' field.

Figure D.2. Default "since" date loaded at start-up.

In this example case, the intake occurred on February 24th, 1988, and so this is the appropriate value for the **Reference Date**. The date of the intake is entered directly in the "**Time (d) since**" dialog box (Figure D.3). The source data did not give the time-of-day. If no value for the hh:mm (time-of-day) of the intake is entered, IMBA Expert™ OCAS/ORAU-Edition assigns this as 00:00 (midnight).

The 'Units' dialog box is shown. It has 'Specify Time As' with 'Date' selected and 'Time (d) since' with a date field set to 2/24/1988. A red box labeled 'Intake (IR 1)' shows a value of 0 Bq. Below the date field, a message states: 'This date corresponds to time = 00:00:00'. To the right is an 'Associated Radionuclide' field.

Figure D.3. Entering the Reference Date.

Since in this example, the bioassay measurements are tabulated with their collection **Date**, it is convenient at this point to switch the "**Specify Time As**" **Units** to "**Date**" (Figure D.4). This switch from "**Time**" to "**Date**" will be passed automatically to the **Bioassay Calculations** screen and **data tables**.

The 'Units' dialog box is shown. It has 'Specify Time As' with 'Date' selected and 'Time (d) since' with a date field set to 2/24/1988. Below the date field, a message states: 'This date corresponds to time = 00:00:00'. To the right is an 'Associated Radionuclide' field.

Figure D.4. Switching the Units of Time to Date.

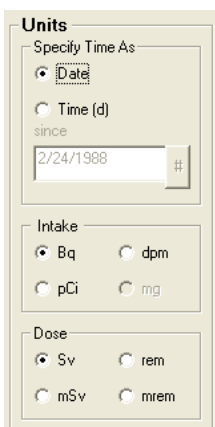
Notice that the "**Start Time (d)**" value of "0" (Figure D.4) has now automatically switched to display the "**Start Date**" as "2/24/1988" - the value entered as the **Reference Date** before the switch of time units.



Key Tip: Always set the **Reference Date** for each case study - in the "**Time (d) since**" dialog box ("**Units**" sub-panel in the **Main Screen**).

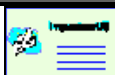
D.2.3. Reference Activity Units for Single Intake

In **IMBA Expert™ OCAS/ORAU-Edition**, the estimated **Intake** has the same **Unit of activity** as the measured (or predicted) **bioassay quantity**. As with the **Unit of Time**, the **Unit of Activity** is selected in the **Main Screen** (Figure D.5). For this example case, the whole-body activity results are tabulated as **Bq**. Therefore, the required **Unit of Activity** is "**Bq**."



The screenshot shows a 'Units' dialog box with three sections: 'Specify Time As' (radio buttons for 'Date' and 'Time (d)', with 'Date' selected), 'Intake' (radio buttons for 'Bq', 'dpm', 'pCi', and 'mg', with 'Bq' selected), and 'Dose' (radio buttons for 'Sv', 'rem', 'mSv', and 'mrem', with 'Sv' selected). A date field shows '2/24/1988'.

Figure D.5. Selecting the **Unit of activity (Intake and Bioassay Quantity)** as "**Bq**."



Warning: **IMBA Expert™ OCAS/ORAU-Edition** works with the **primary bioassay quantity** - which for urinary or fecal excretion is the average **excretion rate** over a prescribed collection period (and not the amount of activity in each sample). So, urinary and fecal bioassay measurements must ALWAYS be entered as the **amount of activity in the sample** (in the selected unit) **divided by the collection period (in d)**.

D.2.4. Selecting the Required Model Parameters

Before you can carry out any calculations with **IMBA Expert™ OCAS/ORAU-Edition**, you MUST define all of the necessary **Model Parameters**. It is most efficient to do this while you are still in the **Main Screen** - although (if you forget to do this) it is very easy and quick to switch backwards and forwards between the **Bioassay Calculations** screen and the **Main Screen** (with a single *click*).

To estimate an Intake (by inhalation) from a measured **Bioassay Quantity**, you must define all the following **Model Parameters** - as indicated by the "red" buttons in Figure D.6:

- **Bioassay** model.
- **Deposition** model.
- **Particle Transport** model.
- **Absorption** model.
- **GI-Tract** model.

If you **omit** defining any of these models, then **IMBA Expert™ OCAS/ORAU-Edition** will **prompt** you for each missing model definition **before** proceeding with a calculation.



Figure D.6. Bioassay button for selecting the **Bioassay Model**.

Bioassay model

For the Bioassay model, *select* the "**Standard Co Model**" for **whole-body retention** (Figure D.7):

- *select* "**Whole body**" as the **Bioassay Function** - this will already have been defined if you had previously selected **Whole body** in the **Bioassay Quantity** window (**Bioassay Calculations** screen);
- *click* the "**LOAD ICRP DEFAULTS**" button;
- *click* "**OK**."

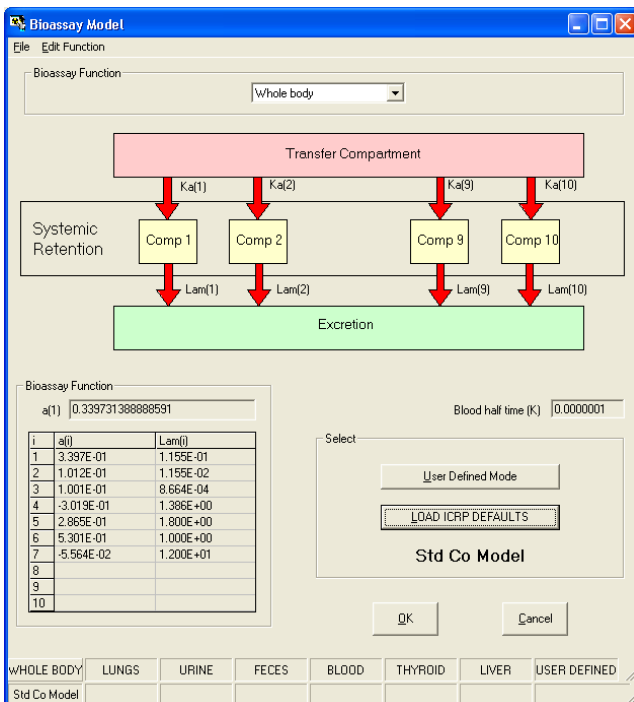


Figure D.7. Standard Co Model for **Whole body** selected as the **Bioassay Model**.

Deposition model

For the Deposition model, select the "Light worker" (Figure D.8):

- click the "**L**OAD ICRP DEFAULTS" button;
- click "**O**K."

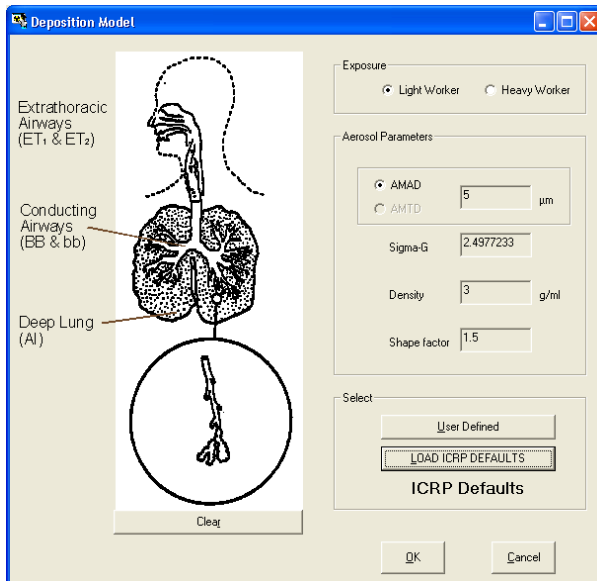


Figure D.8. Selecting the Deposition Model for a Light worker.

Particle transport model

For the Particle Transport model (Figure D.9):

- click the "**L**OAD ICRP DEFAULTS" button;
- click "**O**K."

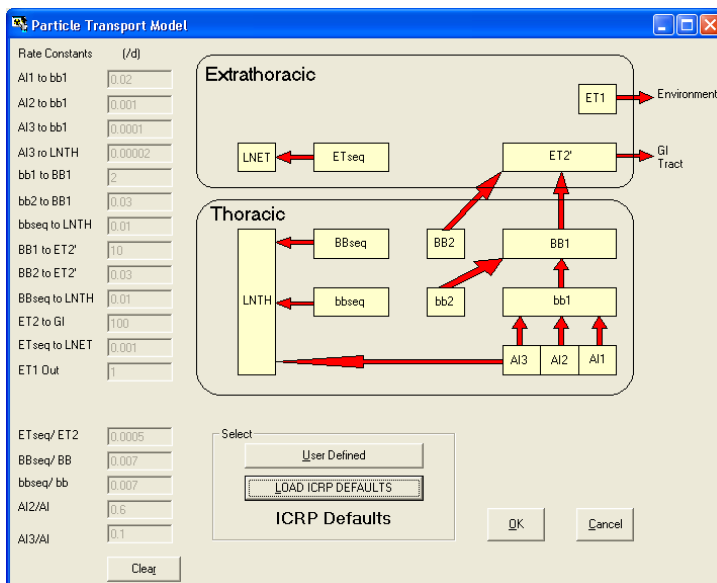


Figure D.9. Selecting the ICRP Default Particle Transport Model.

Absorption model

For the Absorption model, select the **Type M ICRP Default** model (Figure D.10):

- click the "**Type M**" button;
- click "**OK**."

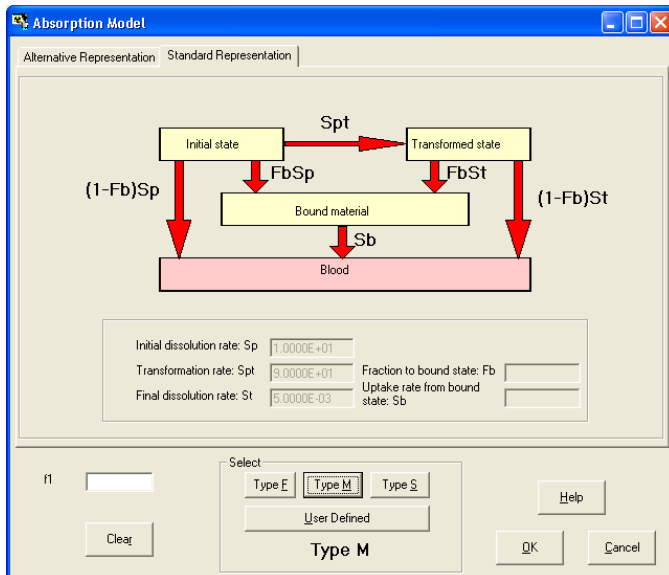


Figure D.10. Selecting the **Type M Absorption Model**.

To select an appropriate (ICRP-recommended) value of f_1 :

- click the "**Help**" button (Figure D.10);
- select the "**Abs.: M**" row (Figure D.11);
- click "**OK**."

Abs.	f1	ICRP Source	Chemical Form
F	0.1	71	
M	0.1	71	Recommended default in the absence of specific information
S	0.01	71	
M	0.1	68	Unspecified compounds
S	0.05	68	Oxides, hydroxides, halides and nitrates
Ing	0.1	68	Unspecified compounds
Ing	0.05	68	Oxides, hydroxides and inorganic compounds

Note: only the absorption parameters are entered. NOT the default AMAD or route of intake.

Figure D.11. Selecting the **ICRP-recommended value of f_1** .

GI-Tract model

For the GI-Tract model, select **LOAD ICRP DEFAULTS** (Figure D.12):

- click the "**LOAD ICRP DEFAULTS**" button;
- click "**OK**."

Figure D.12. Selecting the ICRP Default GI-Tract Model.

This completes the definition of ALL **Model Parameters** required to calculate the **Intake** of ^{60}Co in the IAEA (1999) example case.

Key Tip: You can **short-cut** the process of loading each of the above **Model Parameters** individually by clicking the "**ICRP Defs LOAD**" *tool button*. You will then be prompted to choose the **Absorption Model** and value of f_1 .

D.2.5. Selecting the Intake Regime (IR1)

By default, **IMBA Expert™ OCAS/ORAU-Edition** sets up a **Single Intake Regime (IR1)** - as an **Acute Inhalation** (Figure D.13). At this point no value of the **Intake** has been set (or calculated).

Figure D.13. IR1 defined (by default) as Acute Inhalation.

D.2.6. Selecting Whole-Body as Bioassay Quantity

The previous steps were carried out in the **Main Screen**. You select the **Bioassay Quantity** in the **Bioassay Calculations** screen. From the **Main Screen** you:

- Click the "**Bioassay Calculations**" *button* (bottom-right-corner of the **Main Screen**) - to open the **Bioassay Calculations** screen.

- In the top **Bioassay Quantity** window (set as "Table" by default), select "Whole body" from the drop-down list box (Figure D.14).

This "opens" the first **Bioassay Quantity** window to **display** in that window a **Table** containing both **measured** whole-body activity data (on a **blue background**) and **predicted** whole-body activity data (on a **green background**).

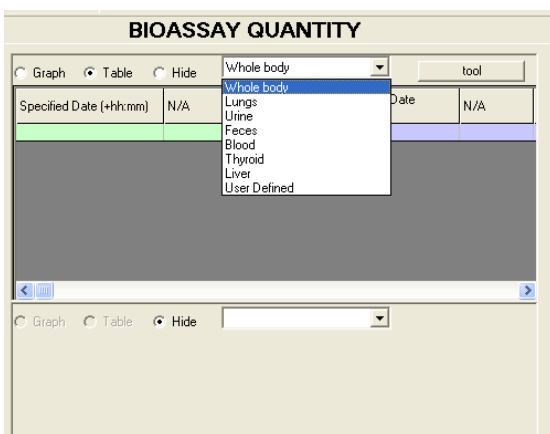


Figure D.14. Drop-down **Bioassay Quantity** list box.

Note: When it is first opened, the data **Table** in the **Bioassay Quantity** window has only one row. This window is designed to display data values, and NOT for data entry. Since no data have yet been entered, there are no data to display at this stage. The "**tool**" button opens the **Table Tool** for your selected **Bioassay Quantity**. This provides the **tools** that you will use to *enter* (and/or *edit*) the **bioassay data** – in the next step.

Tip: Use the **scroll bar** below the open **Bioassay Quantity** window to **view** additional columns (to the right) that are related to **measured bioassay data**.

D.2.7. Entering the Measurement Data

IMBA Expert™ OCAS/ORAU-Edition provides a "**Table Tool**" in the form of an expanded data table with various editing and automated data entry functions.

Opening the Table Tool

Once you have *selected* the **bioassay quantity** for display in the **Bioassay Quantity** window, the "**tool**" button (in the top-right-corner) is activated - see Figure D.15. *Click* this "**tool**" button to *open* the **Table Tool**. This will enable you to *enter* (and/or *edit*) the **whole-body activity data**.

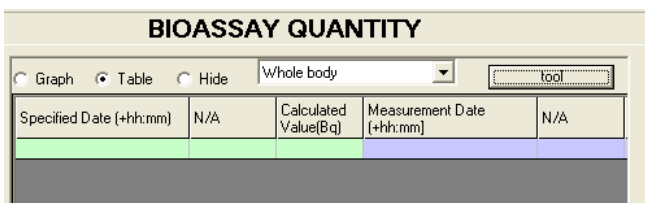


Figure D.15. **Bioassay Quantity** window set to hold "Whole body" data - with active "**tool**" button.

“How to use the Table Tool” to enter the data is described in the **User Manual** (see Section 4.4 under **“HOW TO USE THE BIOASSAY CALCULATIONS SCREEN”**). For this example, in the **Table Tool**, you need to:

1. Enter the eight (paired) values of **“Measurement date”** and **“Whole-body activity (Bq)”** given earlier in **Table D.1** (Section D.2) – **blue** data columns **#1** and **#3**, respectively.
2. Enter **“Real”** in all eight rows of data column **#4** – to signify that these are all real (reliable) measurements.
3. Enter a (hypothetical) **“Uniform Relative”** error of **“0.1”** in all eight rows of data column **#5** – to signify the assumption of a uniform relative error on all measured values.
4. Enter **“NORM”** in all eight rows of data – to signify that the error in the measured quantity is assumed to be normally distributed.

The completed **Bioassay Quantity** table will then be displayed as shown in Figure D.16.

Measurement Date (+hh:mm)	N/A	Measurement Value(Bq)	Data Type	Measurement Error	Error Distribution
2/25/1988		2.720E+03	Real	2.720E+02	NORM
3/1/1988		1.150E+03	Real	1.150E+02	NORM
3/11/1988		1.010E+03	Real	1.010E+02	NORM
3/28/1988		7.900E+02	Real	7.900E+01	NORM
5/16/1988		4.820E+02	Real	4.820E+01	NORM
8/11/1988		3.580E+02	Real	3.580E+01	NORM
11/29/1990		7.800E+01	Real	7.800E+00	NORM
2/19/1992		3.500E+01	Real	3.500E+00	NORM

Figure D.16. Table of **Bioassay Data** for example case of single intake of ^{60}Co .

D.2.8. Graphing the Data

IMBA Expert™ OCAS/ORAU-Edition provides a **“Graph Tool”** in the form of an expanded graphical display with full facilities for setting up the type of graph (linear or logarithmic), ordinate and abscissa scales, etc.

Opening the Graph Tool

Select **“Graph”** and **“Whole body”** for display in the second **Bioassay Quantity** window (Figure D.17). Then click the **“tool”** button to open the **Graph Tool**.

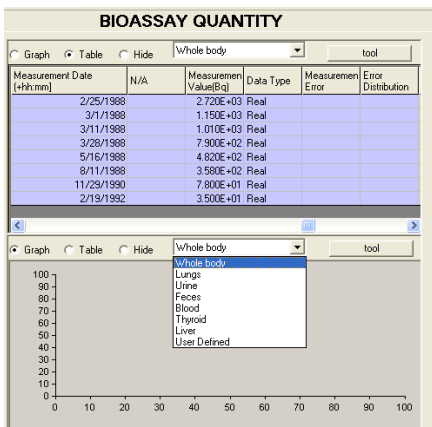


Figure D.17. Opening a **Graph** window for the **Whole body** bioassay quantity.

"How to use the Graph Tool" to set up the graph is described the **User Manual** (see Section 4.5 under "HOW TO USE THE BIOASSAY CALCULATIONS SCREEN"). For this example, in the **Graph Tool**, you need to:

1. Click the "Select Axes Automatically" button.
2. In the "Plot" sub-panel, check;
 - the "Data – Plot" box
 - the "Data – Error Bars" box
 - the "Fit – Plot" box.

At this stage, the **data** and **error bars** will appear in the **Bioassay Quantity graph** window as shown in Figure D.18.

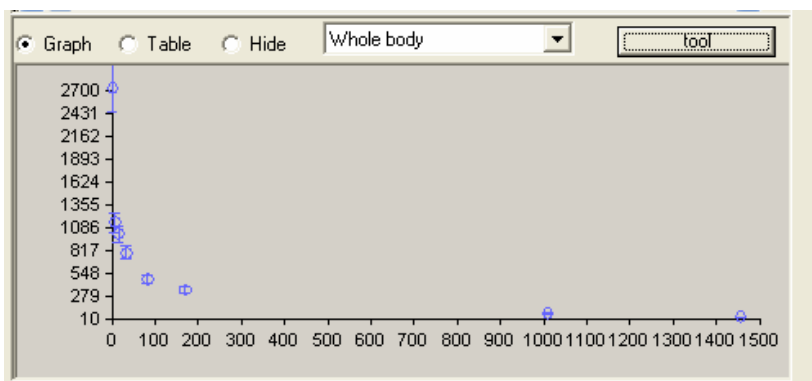


Figure D.18. Graph of **Bioassay Data** for example case of single intake of ^{60}Co .



Warning: You CANNOT open the **Graph Tool** until you have entered (or read in from a file) a value of "Measurement Error" - for every tabulated "Measurement Value". If you attempt to do this, you will be prompted to complete the data entry.

D.2.9. Selecting Bioassay Data to Use - and Calculating Intake

Before you can calculate the amount of **Intake**, you MUST first **Select which data to use**. In the "CALCULATION" sub-panel (**Bioassay to Intake** - Figure D.19):

- check the **Whole body** box.

If you forget to do this, you will be prompted. To calculate the **maximum likelihood estimate** of the **Intake** amount:

- click the "Start Calculation" button (Figure D.19).

This will:

- display automatically the **Intake** amount for the single **Intake Regime (IR1)**;
- plot automatically the corresponding **fit** to the **data points** (see Figure D.19) - provided that the "Plot Fit" box was checked in the **Graph Tool**.

In this example, with the selected values of **Model Parameters**, the calculated **Intake** amount is **10,341 Bq**.

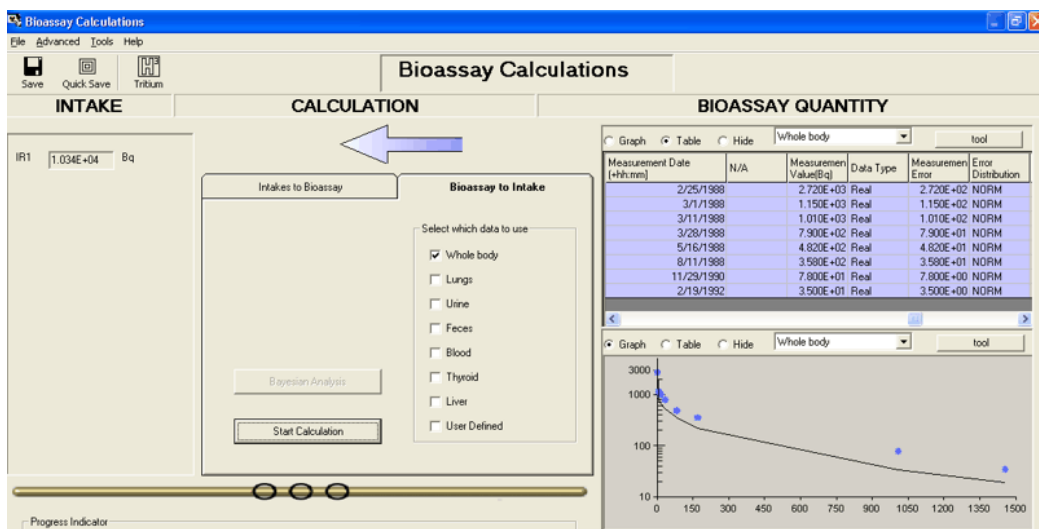


Figure D.19. Calculated Intake amount with corresponding “best fit” to the data.

You will see from the **Table** and **Figure** displayed in the **Bioassay Quantity** windows (Figure D.19) that the **fit** to data points is generally poorer than the assumed measurement errors. This fit can be improved quite readily, by **reviewing**, and if necessary making **reasonable changes** to, one or more of the assumed **Model Parameters** (see the following sub-section).

D.2.10. Improving the Data Fit

In this example case (single intake of ^{60}Co by inhalation), the **fit** to the data is **clearly improved** by varying the assumed aerosol **Activity Median Aerodynamic Diameter (AMAD)** from the **5- μm default value** recommended by **ICRP** - to an **AMAD of 1 μm** (with $\sigma_g = 2.47$). The resulting **improved data fit** (at least to the earliest 6 data points) is shown in Figure D.20. The corresponding (better) estimate of the **Intake** amount is **9,805 Bq**.

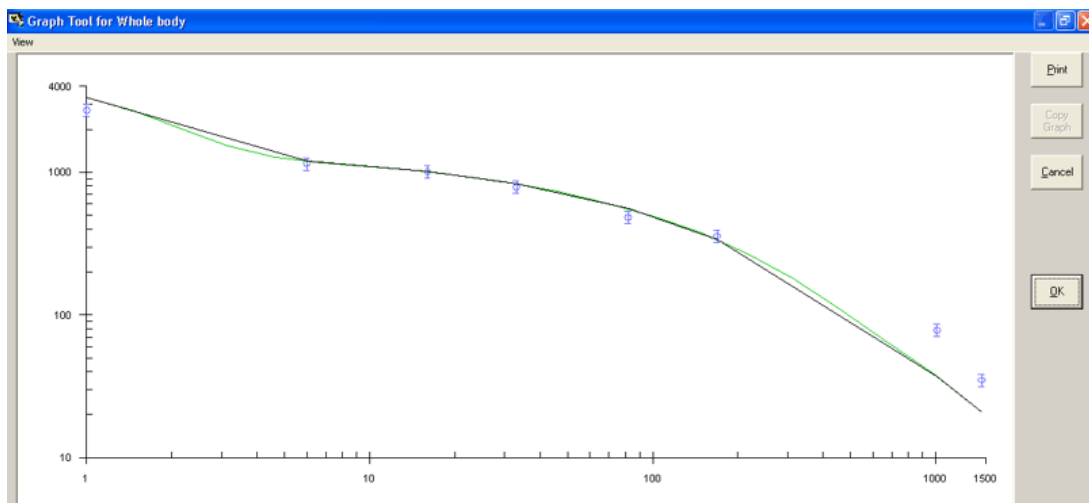


Figure D.20. Improved data fit obtained by changing the value of aerosol AMAD.



Tip: As an instructive **exercise**, try **varying** other **Model Parameters** (within reasonable ranges) to **examine** their effect on the **data fit**.

D.3. Estimating Multiple Intakes

This example is taken from *Miller et al. (1999)* - see their Appendix 2. The data are urinary excretion measurements of ^{238}Pu in 37 samples taken from March 15th, 1968 through May 28th, 1979. The worker concerned had several intakes (by inhalation) of mixed $^{239}\text{Pu}/^{238}\text{Pu}$:

1. In the mid-1950s - and assumed for analysis purposes to have occurred on June 9th, 1945.
2. On May 8th, 1971.
3. At some unknown time between the routine sampling dates of September 22nd, 1971 and September 18th, 1972.

In their analysis, Miller et al. assigned the date of the third intake as March 21st, 1972 (mid-way between the prior- and post-intake samples). No information about the physical properties of the $^{239}\text{Pu}/^{238}\text{Pu}$ material (or aerosol) was presented. The urinalysis results are given in Table D.2.

Table D.2. ^{238}Pu urinalysis results.

Collection date	Excretion rate (mBq d ⁻¹) $\pm$ 1 SD
March 15, 1968	1 $\pm$ 0.9
June 13, 1968	1.8 $\pm$ 0.9
September 13, 1968	0.3 $\pm$ 0.9
December 13, 1968	4.8 $\pm$ 2
March 20, 1969	0 $\pm$ 0.9
December 18, 1969	0 $\pm$ 0.9
March 19, 1970	0 $\pm$ 0.9
June 18, 1970	0.5 $\pm$ 0.9
September 24, 1970	0.5 $\pm$ 0.9
March 18, 1971	1.2 $\pm$ 0.7
June 29, 1971	4.1 $\pm$ 0.7
September 22, 1971	2.2 $\pm$ 0.5
September 18, 1972	12.9 $\pm$ 1.6
December 8, 1972	7.5 $\pm$ 1.1
March 15, 1973	2 $\pm$ 0.4
June 27, 1973	3 $\pm$ 0.6
September 17, 1973	2.7 $\pm$ 0.5
December 21, 1973	3.1 $\pm$ 0.6
March 21, 1974	1.1 $\pm$ 0.4
June 17, 1974	3.8 $\pm$ 0.7
September 16, 1974	2.1 $\pm$ 0.5
December 18, 1974	1.5 $\pm$ 0.4
March 17, 1975	2 $\pm$ 0.4
June 16, 1975	1.1 $\pm$ 0.4
September 19, 1975	0.8 $\pm$ 0.4
December 12, 1975	1 $\pm$ 0.4
March 17, 1976	1.2 $\pm$ 0.4
July 2, 1976	1.4 $\pm$ 0.4
September 12, 1976	1.4 $\pm$ 0.4
December 8, 1976	0.5 $\pm$ 0.4
June 24, 1977	1 $\pm$ 0.4
September 15, 1977	0.4 $\pm$ 0.4
September 1, 1978	2.2 $\pm$ 0.5
October 20, 1978	0.3 $\pm$ 0.4
January 18, 1979	0.9 $\pm$ 0.4
April 20, 1979	0.4 $\pm$ 0.4
May 28, 1979	1.6 $\pm$ 0.4

The following steps (in the listed order) are recommended for making an **initial estimate** of the amounts of the three separate intakes in this example.

1. Select the Indicator Nuclide - in the **Main Screen**.
2. Define the Reference Date - in the **Main Screen**.
3. Select the Reference Activity Units - in the **Main Screen**.
4. Select the Common Model Parameters to be used for **all IRs** - in the **Main Screen**.
5. Select the Number of Intake Regimes (IRs) - in the **Main Screen**.
6. Select the option for Independent Model Parameters for all IRs - in the **Main Screen**.
7. Define the Date of Each Intake - in the **Main Screen**.
8. Select - in the **Bioassay Calculations** screen - the **Bioassay Quantity** as "Urine" (for display in the top **Bioassay Quantity** window).
9. Enter the bioassay data - using the data entry "tool" in the **Bioassay Quantity** window.
10. Graph the bioassay data - using the graph set up "tool" in **Bioassay Quantity** window.
11. Select which bioassay data to use ("**Urine**") in the **CALCULATION** sub-panel.
12. Click the "**Start Calculation**" button.

When you have completed these steps - and made your initial estimate of the amounts of each intake - you will start the **iterative** process of **refining** these estimates by comparing the **predicted** urinary excretion rates with the **measured** values.

	Tip: When you are familiar with the operation of IMBA Expert™ OCAS/ORAU-Edition , you will find that the initial Steps 1 through 10 can be performed in any order (to suit your own working style) - just as long as ALL of the parameter and data values have been defined BEFORE you click the " Start Calculation " button.
	Important: If you have missed a step, IMBA Expert™ OCAS/ORAU-Edition will prompt you to carry this out - but only if the required data values are missing (null).
	Warning: It is your responsibility to check that ALL of the model parameters have been set to your specific requirements. IMBA Expert™ OCAS/ORAU-Edition will use whatever values are in memory when you click the " Start Calculation " button.

D.3.1. Indicator Nuclide for Multiple Intakes

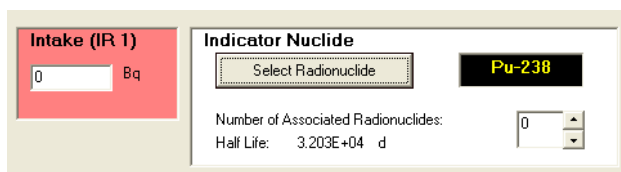


Figure D.21. Selecting the Indicator Nuclide (^{238}Pu).

Select the **Indicator Nuclide** (^{238}Pu in the example case) from the top-right-corner of the **Main Screen** (Figure D.21). **IMBA Expert™ OCAS/ORAU-Edition** will then be able to select automatically the **bioassay model(s)** appropriate for plutonium, and automatically take into account the **radioactive half-life** of ^{238}Pu .

	Tip: In this example case, we are using bioassay data to calculate intake(s) . Therefore, it is NOT necessary to enter a (hypothetical) value in the displayed "Intake (IR 1)" dialog box. IMBA Expert™ OCAS/ORAU-Edition will automatically display the calculated values of Intake(s) in their respective dialog boxes.
---	--

D.3.2. Reference Date for Multiple Intakes

This is a KEY parameter - especially for cases where more than one intake is being analyzed. **IMBA Expert™ OCAS/ORAU-Edition** keeps track of all **Intakes** and **bioassay measurements** on a common timescale. All events are timed with respect to a single **Reference Date** (and **time-of-day**, if necessary). The **Reference Date** is defined in the **Main Screen** (Figure D.22). The **IMBA System** must always have a reference date - even if you are working entirely in the **Time (d)** mode - so a **default** value (January 1st, 1980) is loaded at start-up.

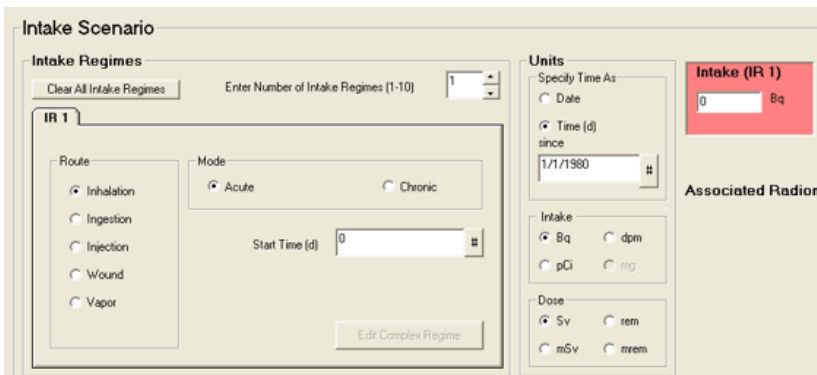


Figure D.22. Default "since" date loaded at start-up.

In this example case, the earliest date of interest is June 9th, 1945, and so this is the appropriate value for the **Reference Date**. This is entered directly in the "**Time (d) since**" dialog box (Figure D.23).

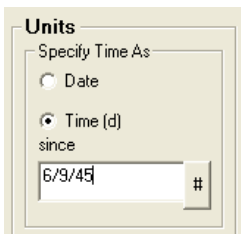


Figure D.23. Entering the Reference Date.

Since in this example, the bioassay measurements are tabulated with their collection **Date**, it is necessary at this point to switch the "**Specify Time As**" Units to "**Date**" (Figure D.24). This switch from "**Time**" to "**Date**" will be passed automatically to the **Bioassay Calculations** screen and **data tables**.

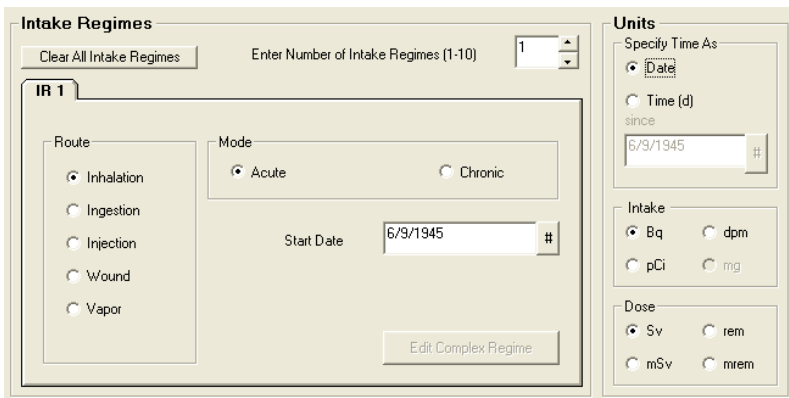


Figure D.24. Switching the Units of Time to Date.

Notice that the "Start Time (d)" value of "0" (Figure D.24) has now automatically switched to display the "Start Date" as "6/9/1945" - the value entered as the **Reference Date** before the switch of time units.



Key Tip: Always set the **Reference Date** for each case study - in the "Time (d) since" dialog box ("Units" sub-panel in the **Main Screen**).

D.3.3. Reference Activity Units for Multiple Intakes

In **IMBA Expert™ OCAS/ORAU-Edition**, the estimated **Intake** has the same **Unit of activity** as the measured (or predicted) **bioassay quantity**. As with the **Unit of Time**, the **Unit of Activity** is selected in the **Main Screen** (Figure D.25).

Figure D.25. Selecting the **Unit of activity (Intake and Bioassay Quantity)** as "Bq."



Warning: **IMBA Expert™ OCAS/ORAU-Edition** works with the **primary bioassay quantity** - which for urinary or fecal excretion is the average **excretion rate** over a prescribed collection period (and not the amount of activity in each sample). So, urinary and fecal bioassay measurements must **ALWAYS** be entered as the **amount of activity in the sample** (in the selected unit) **divided by the collection period (in d)**.

D.3.4. Selecting the Common Model Parameters for All IRs

Before you can carry out any calculations with **IMBA Expert™ OCAS/ORAU-Edition**, you **MUST** define all of the necessary **Model Parameters**. It is most efficient to do this while you are still in the **Main Screen** - although (if you forget to do this) it is very easy and quick to switch backwards and forwards between the **Bioassay Calculations** screen and the **Main Screen** (with a single *click*).



You can "**pre-set**" **ALL** model parameters to "**ICRP Default**" values - with a single *click* of the "**ICRP DEFS Load**" *button*.



Then, as you open additional **Intake Regimes (IRs)**, the "**Default**" models will be loaded automatically - so that you won't have to carry out all of the individual steps listed below (for each **IR**). In general, it is much quicker to *load* (first) **ALL ICRP Default** model parameter values (for **ALL IRs**) - and then *change* only the relatively few parameters values that are **specific** to your case.

To estimate an **Intake** (by inhalation) from a measured **Bioassay Quantity**, you must define all the following **Model Parameters** - as indicated by the "red" buttons in Figure D.26:

- **Bioassay** model.
- **Deposition** model.
- **Particle Transport** model.
- **Absorption** model.
- **GI-Tract** model.

If you **omit** defining any of these models, then **IMBA Expert™ OCAS/ORAU-Edition** will **prompt** you for each missing model definition **before** proceeding with a calculation.

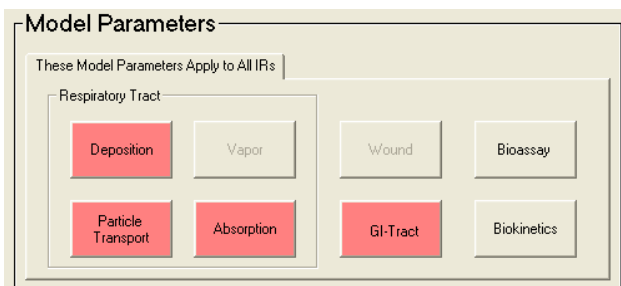


Figure D.26. Bioassay button for selecting the **Bioassay Model**.

Bioassay model

For the Bioassay model, *select* the "**Standard Pu Model**" for **urinary excretion** (Figure D.27):

- *select* "**Urine**" as the **Bioassay Function** - this will already have been defined if you had previously selected **Urine** in the **Bioassay Quantity** window (**Bioassay Calculations** screen);
- *click* the "**LOAD ICRP DEFAULTS**" button;
- *click* "**OK**."

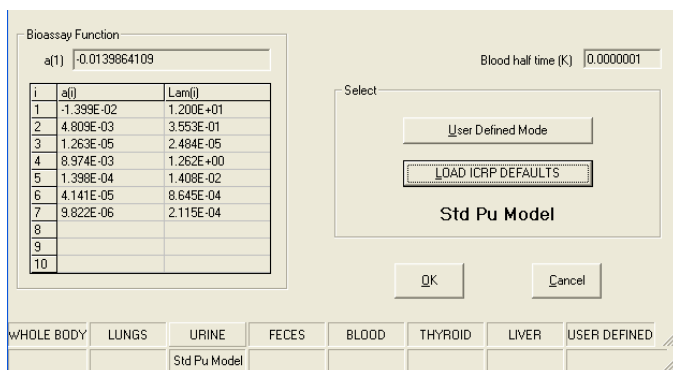


Figure D.27. **Standard Pu Model** for **Urine** selected as the **Bioassay Model**.

Deposition model

For the Deposition model, *select* the "**Light worker**" (Figure D.28):

- *click* the "**LOAD ICRP DEFAULTS**" button;
- *click* "**OK**."

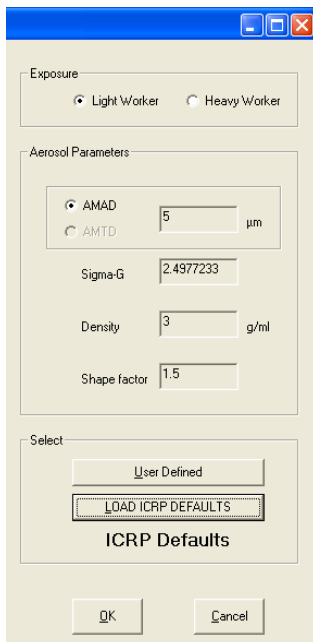


Figure D.28. Selecting the **Deposition Model** for a **Light worker**.

Particle transport model

For the Particle Transport model (Figure D.29):

- click the "LOAD ICRP DEFAULTS" button;
- click "OK."

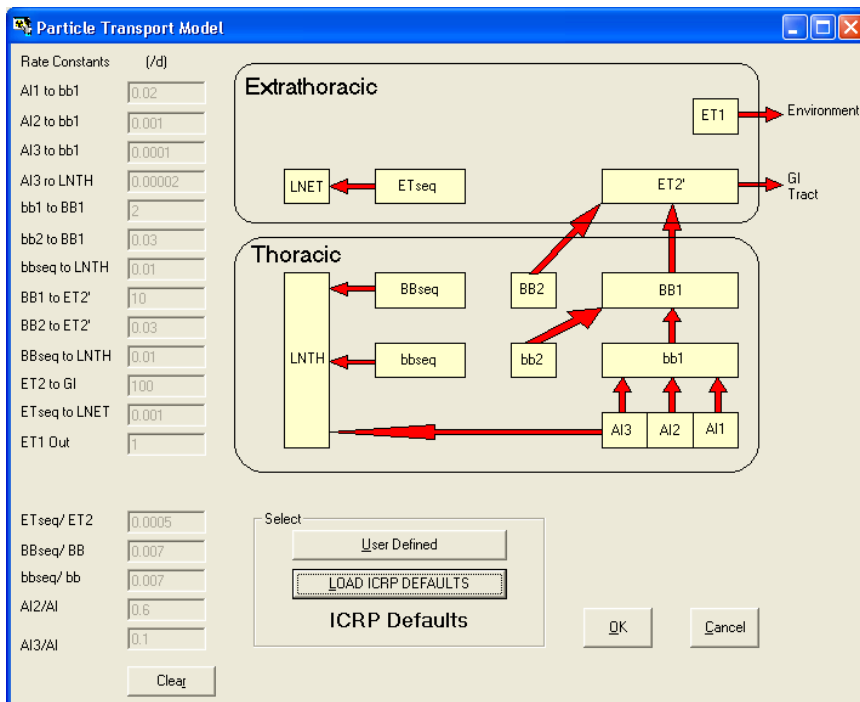


Figure D.29. Selecting the ICRP Default Particle Transport Model.

Absorption model

For the Absorption model, select the **Type M ICRP Default** model (Figure D.30):

- click the "**Type M**" button;
- click "**OK**."



Figure D.30. Selecting the Type M Absorption Model.

To select an appropriate (ICRP-recommended) value of f_1 :

- click the "**Help**" button (Figure D.30);
- select the "**Abs.: M**" row (Figure D.31);
- click "**OK**."

Abs.	f1	ICRP Source	Chemical Form
F	0.0005	71	
M	0.0005	71	Recommended default in the absence of specific information.
S	0.00001	71	
M	0.0005	60	Unspecified compounds
S	0.00001	68	Insoluble oxides
Ing	0.0005	68	Unspecified compounds
Ing	0.0001	60	Nitrates
Ing	0.00001	68	Insoluble oxides

Note: only the absorption parameters are entered. NOT the default AMAD or route of intake.

Figure D.31. Selecting the ICRP-recommended value of f_1 .

GI-Tract model

For the GI-Tract model, select **LOAD ICRP DEFAULTS** (Figure D.32):

- click the "**LOAD ICRP DEFAULTS**" button;
- click "**OK**."

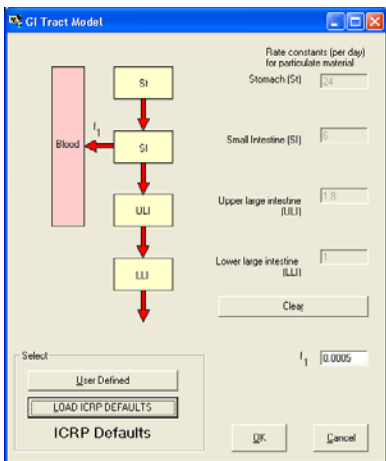


Figure D.32. Selecting the ICRP Default GI-Tract Model.

This completes the definition of ALL **Model Parameters** required to calculate the (3) **Intakes** of ^{238}Pu in the *Miller at al. (1999)* example case.



Key Tip: Don't forget that you can **short-cut** the process of loading each of the above **Model Parameters** individually by *clicking* the "**ICRP DEFS LOAD**" tool button. You will then be prompted to choose just the **Absorption Model** (i.e., type of absorption behavior) and the value of f_1 .

D.3.5. Selecting the Number of Intake Regimes (IRs)

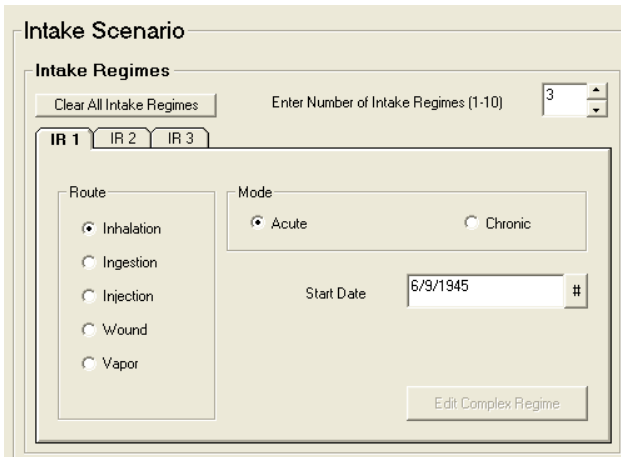


Figure D.33. Selecting 3 separate Intake Regimes (IRs).

In the "**Intake Scenario**" panel ("**Intake Regimes**" sub-panel) simply *enter* the required number of **individual** (separate) **intake events** in the dialog box.

D.3.6. Selecting Independent Model Parameters

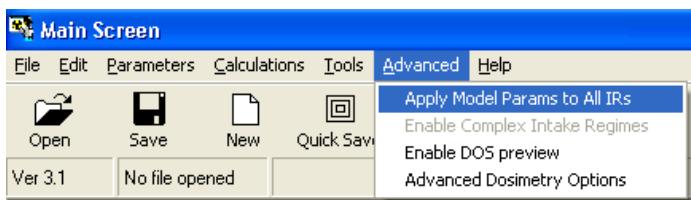


Figure D.34. Un-checking "Apply Model Params to All IRs" in the "Advanced" menu.

By default, **IMBA Expert™ OCAS/ORAU-Edition** applies all of the defined **Model Parameters** to **All Intake Regimes (IRs)**. If you want to **specify independently** ANY parameter value (e.g., the **date/time** of the **Intake**) for ANY individual **IR**, you **MUST** first *un-check* the **default** condition in the "**Advanced**" menu (Figure D.34).



Note: When you have *selected* **more than 1 Intake Regime** - AND you have *un-checked* the **default "Apply Model Params to All IRs,"** the appropriate **number of tabs** will appear automatically in the "**Model Parameters**" sub-panel (Figure D.35). You can then proceed to set up (or modify) ANY **model parameter** for ANY **individual IR#**.

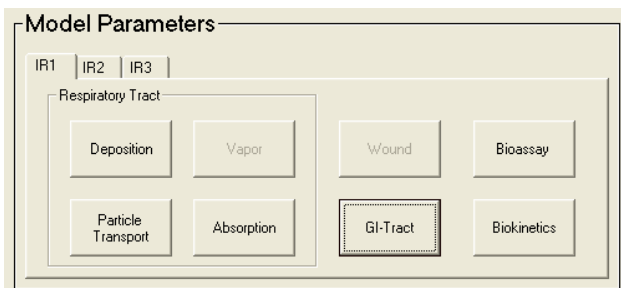


Figure D.35. Individual IR# tabs for setting up Model Parameters specific to each IR.

D.3.7. Defining the Date of Each Intake

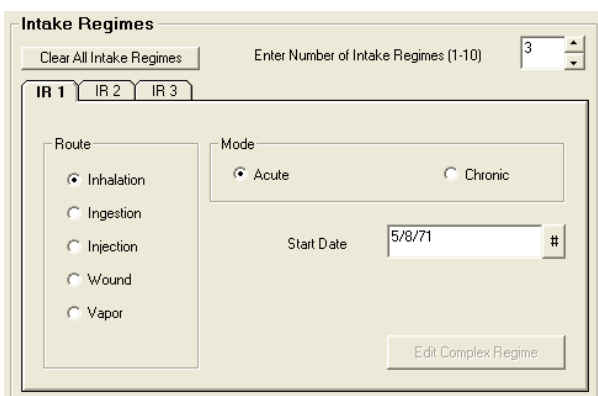


Figure D.36. Setting the Date of IR 2 as May 8th, 1971.

Once you have specified **independent model parameters** for **all IRs**, you simply click on each **IR # tab** displayed in the "Intake Regimes" sub-panel to *specify* the **intake parameter values** for that IR # (Figure D.36). For the **initial estimate** of the amounts of **each** (acute) Intake:

- enter the "Start Date" of IR 2 as May 8th, 1971;
- enter the estimated "Start Date" of IR 3 as March 21st, 1972.



Note: In this example, all 3 of the intakes are assumed to be "acute." You can, of course, specify "chronic" for ANY intake, as appropriate.

D.3.8. Selecting the Bioassay Quantity

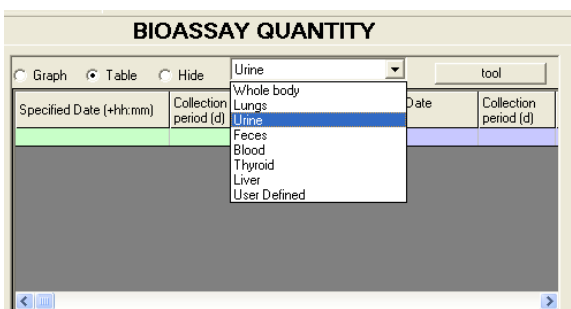
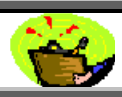


Figure D.37. Drop-down Bioassay Quantity list box.

The previous steps were carried out in the **Main Screen**. You *select* the **Bioassay Quantity** in the **Bioassay Calculations** screen. From the **Main Screen** you:

- Click the "**Bioassay Calculations**" *button* (bottom-right-corner of the **Main Screen**) - to open the **Bioassay Calculations** screen.
- Select the "**Bioassay to Intake**" direction for the **CALCULATION** (indicated by a **blue** arrow) - if you loaded a "**new**" (blank) **Parameter File**, this calculation mode will have been selected already (by **default**).
- In the top **Bioassay Quantity** window (set as "**Table**" by default), select "**Urine**" from the drop-down list box (Figure D.37).

This "**opens**" the first **Bioassay Quantity** window to **display** in that window a **Table** containing both **measured** urinary excretion data (on a **blue background**) and **predicted** urinary excretion data (on a **green background**).

	Note: When it is first opened, the data Table in the Bioassay Quantity window has only one row. This window is designed to display data values, and NOT for data entry. Since no data have yet been entered, there are no data to display at this stage. The " tool " <i>button opens</i> the Table Tool for your selected Bioassay Quantity . This provides the tools that you will use to <i>enter</i> (and/or <i>edit</i>) the bioassay data - in the next step .
	Tip: Use the scroll bar below the open Bioassay Quantity window to <i>view</i> additional columns (to the right) that are related to measured bioassay data .

D.3.9. Data Entry - Multiple Intake Example

IMBA Expert™ OCAS/ORAU-Edition provides a "**Table Tool**" in the form of an expanded data table with various editing and automated data entry functions..

Opening the Table Tool

The **Table Tool** shows all of the data columns (without you having to scroll). When you open this [from a **Bioassay Quantity (BQ)** window], the **Table Tool** will display the same number of rows as the **BQ** window. Initially, only a **default single row** is displayed. Your first task is to open up enough rows to hold all of the **measured bioassay data** that you want to analyze - in this example, **37** values of daily urinary excretion:

- Enter "**37**" in the "**Number of Rows**" dialog box (bottom panel, left-of-center - see Figure D.38).
- Click the "**Apply**" *button* to the right of the dialog box.

	Tip: The number of data rows shown in the Table Tool depends on your screen resolution setting. The minimum recommended screen resolution (1024 X 768) shows 35 rows - as in Figure D.38.
---	---

Specified Date (mm-mm)	Collection period (d)	Calculated Rate(lg/d)	Measurement Date (mm-mm)	Collection period (d)	Measurement Rate(lg/d)	Data Type	Measurement Error	Error Distribution	Theoretical Rate(lg/d)	Chi-Square
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
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34										
35										
36										
37										

Table D.38. Table Tool with 37 rows opened.



Note: For a detailed description of “How to Use the Table Tool” – see the **User Manual** (Section 4.4 under “HOW TO USE THE BIOASSAY CALCULATIONS SCREEN”).

D.3.10. Graphing the Data - Multiple Intakes

IMBA Expert™ OCAS/ORAU-Edition provides a “**Graph Tool**” in the form of an expanded graphical display with full facilities for setting up the type of graph (linear or logarithmic), ordinate and abscissa scales, etc.

Opening the Graph Tool

Select “**Graph**” and “**Urine**” for display in the second **Bioassay Quantity** window. Then *click* the “**tool**” button to open the **Graph Tool** (Figure D.39).

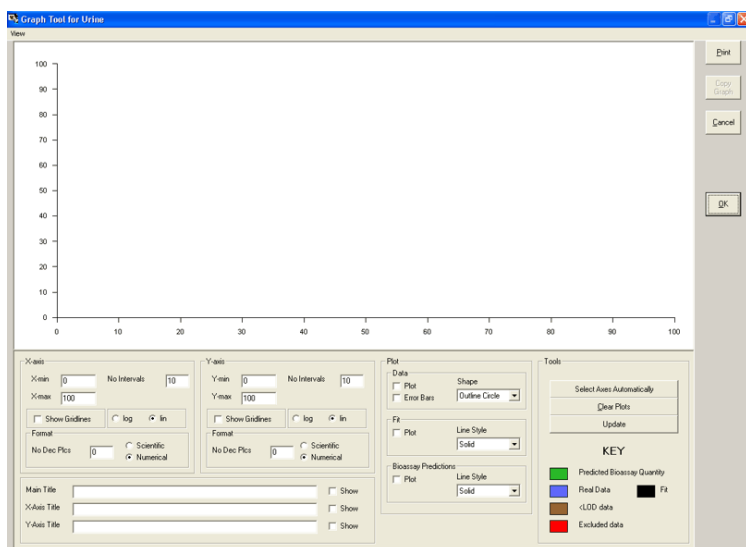


Figure D.39. Opening the **Graph Tool** for the **Urine** bioassay quantity.

Note: For a detailed description of "How to Use the Graph Tool" see the **User Manual** (Section 4.5 under "HOW TO USE THE BIOASSAY CALCULATIONS SCREEN").

D.3.11. Calculating the Intake Amounts

Before you can *calculate* the amounts of each of the **three Intakes**, you **MUST** first *Select which data to use*. In the "CALCULATION" sub-panel (**Bioassay to Intake** - Figure D.40):

- check the **Urine** box.

If you forget to do this, you will be prompted.

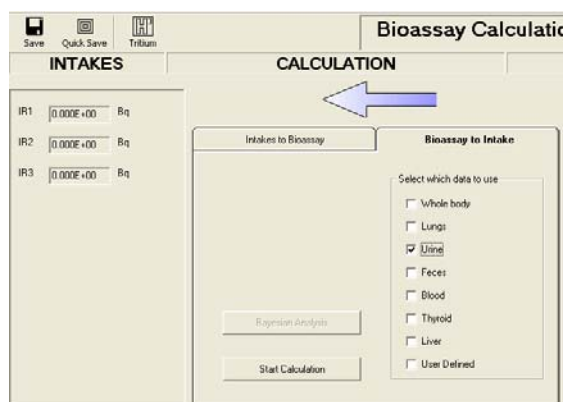


Figure D.40. Selecting **Urine** as the **Bioassay Quantity** to use to estimate the **Intakes**.

To *calculate* the **maximum likelihood** estimate of the **Intake** amounts:

- click the "**Start Calculation**" button (Figure D.40).

This will:

- *display* automatically the **Intake** amounts for all three **Intake Regimes (IR1, IR2 and IR3)**;
- *plot* automatically the corresponding **fit** to the **data points** (see Figure D.41) - provided that the "**Plot Fit**" box was *checked* in the **Graph Tool**.

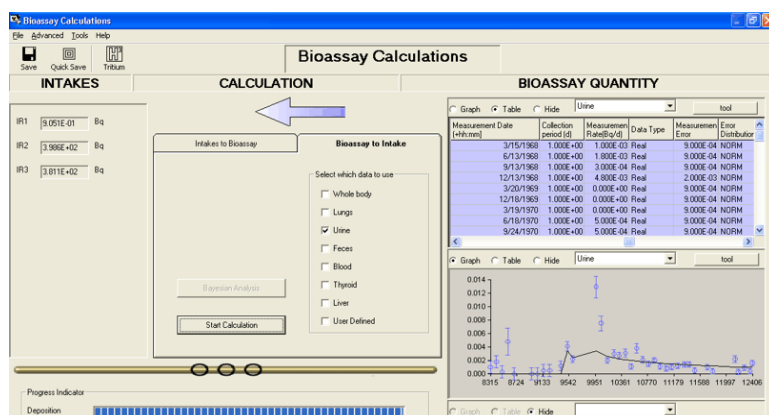


Figure D.41. Calculated **Intakes** with corresponding "**best fit**" to the data (for assumed **Type M** absorption behavior).

In this example, with the selected values of **Model Parameters**, the calculated **Intakes** are:

- **IR1 = 0.91 Bq;**
- **IR2 = 398.6 Bq;**
- **IR3 = 381.1 Bq.**

Figure D.41 shows that the resulting **fit** to data points is poor, especially:

1. in not representing the well defined "**peak**" (from **IR3**) in the measured urine data (with its **subsequent rapid decay**) at **9,963 d**;
2. in predicting "**zero**" urinary excretion (from **IR1 = 0**) prior to the second **intake** (from **IR2**) on May 8th, 1971 (at **9,464 d**).

To improve the "**fit**" to the measured urinary excretion data, it is necessary to *review*, and *modify* appropriately, the assumed **Model Parameters** for each **Intake Regime**.

For example, since the **absorption behavior** of the inhaled material is **unknown**, it is reasonable to **change** this (for **all 3 IRs**), and see the effect on the **data fit**. *Changing the absorption behavior for All IRs to "Type S" - with the associated value of $f_1 = 0.00001$ - and recalculating the intake amounts*, gives the result shown in Figure D.42.

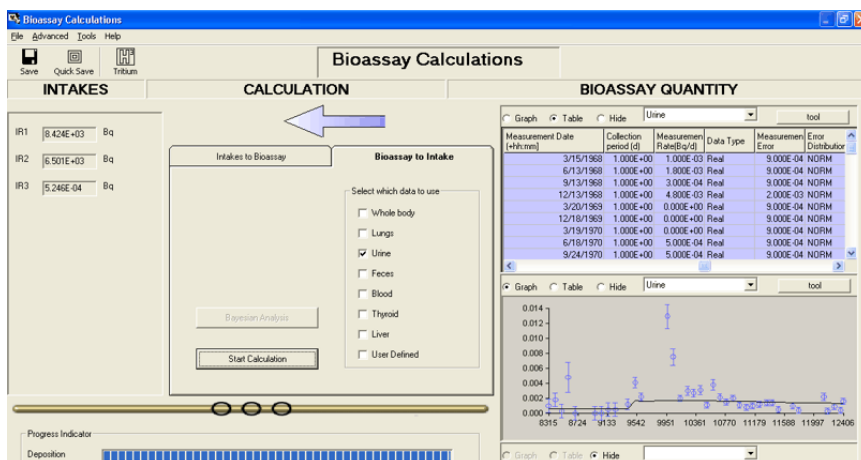


Figure D.42. Calculated **Intakes** with corresponding **best fit** to the data for assumed **Type S** absorption behavior.

Clearly, the assumption of **Type S** absorption behavior gives a **worse** overall fit to the measured urine data than **Type M** (Figure D.41). **Type S** behavior **does** predict a step-wise increase in urinary excretion at **9,464 d** (from **IR2**), and also the presence of **finite excretion** prior to that date (from **IR1**). However:

1. it **CANNOT** fit the observed **sharp increase** in the excretion rate following **IR3**;
2. **NOR** the observed **sharp drops** in the excretion rate following both **IR2** and **IR3**.

Note that changing the assumed absorption behavior also **changes significantly** the "**best estimates**" of the **intake amounts** to:

- **IR1 = 8,424 Bq;**
- **IR2 = 6,501 Bq;**
- **IR3 = 0.0005 Bq.**

D.3.12. Testing the Intake Estimation (Examining the Data Fit)

Although the assumption of **Type M** absorption behavior in the "multiple intake" example gave a **better fit** (Figure D.41) to the measured data than **Type S**, the fit was still **not good**. In order to improve this, **IMBA Expert™ OCAS/ORAU-Edition** provides a further powerful **tool** for **optimizing the data fit**. This is the **"Intakes to Bioassay"** option in the **"CALCULATIONS"** sub-panel. This option enables you to *predict the bioassay quantity* with **sufficient time-resolution** to *examine* in detail the **fit** achieved for **rapidly changing data** (significant observed **"peaks"** in the data).

The first step in **testing** an intake estimation is to switch the **"CALCULATION"** mode from **"Bioassay to Intake"** (blue arrow) to **"Intakes to Bioassay"** (green arrow) - as shown in Figure D.43.

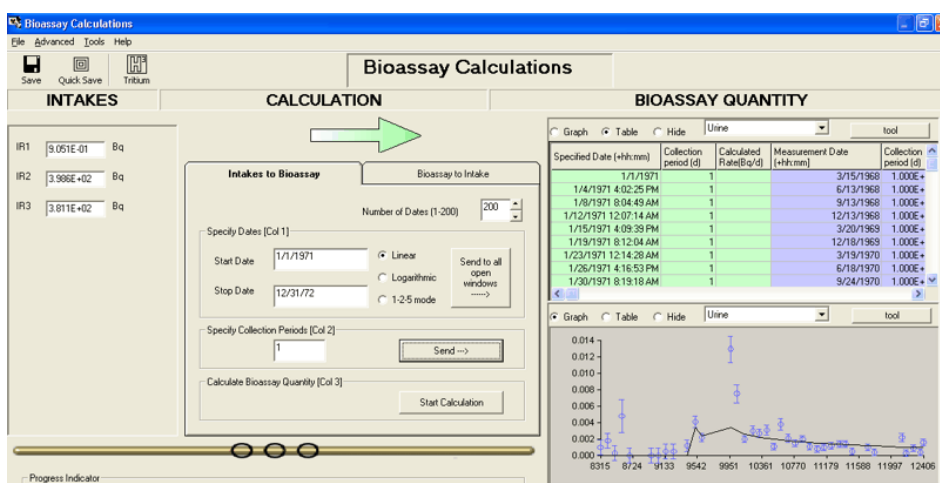


Figure D.43. Setting up a series of times at which to predict the bioassay quantity.

In this example, the measured urinary excretion data exhibited significant **"peaks"** in 1971 and 1972. However, these bioassay data were taken at **"routine"** sampling intervals - and **NOT in response to intake events** (known or suspected). As a result, much of the **early urinary excretion** of relatively soluble plutonium would have been **missed**. The **"Intakes to Bioassay"** option enables this predicted early excretion to be examined on the **same graph plot** as the **measured data**.

For this example (Figure D.43):

- select 200 as the **Number of Dates (1-200)**;
- select **Linear** for the time series;
- specify the **Start Date** as **"1/1/71"**;
- specify the **Stop Date** as **"12/31/72"**;
- click the **"Send to all open windows →"** button;
- enter **"1"** in the **"Specify Collection Periods [Col 2]"** dialog box;
- click the **"Send →"** button.

This will automatically:

1. open 200 rows (green background) in the **Bioassay Quantity** table;
2. enter [in Column 1] the 200 values of **date/time** (at **linear** intervals);
3. enter **"1"** for the **Collection Period** [Column 2] for each of the 200 sample times.

To calculate the predicted amount of urinary excretion for all 200 (hypothetical) samples - for the displayed "**initial**" estimates of the **intake amounts** - and to **display the results** in Column 3 of the table:

- click the "**Start Calculation**" button.

The **predicted values** are shown in Figure D.44.

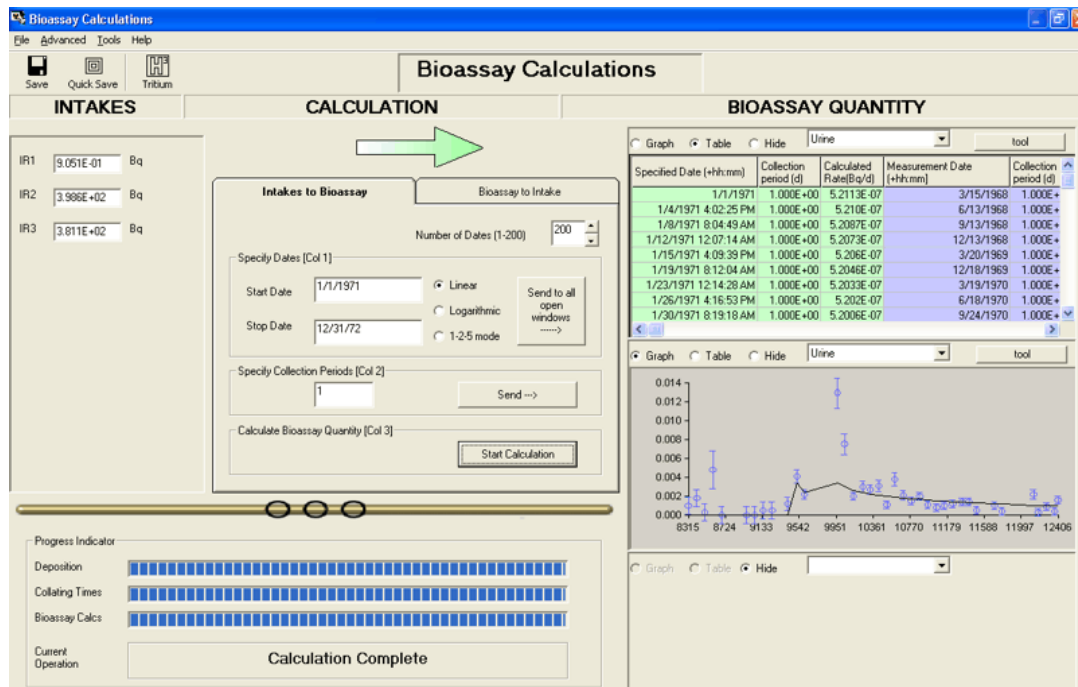


Figure D.44. Predicted bioassay quantity displayed in the **Bioassay Quantity** window.

Warning: If you are using a **slow** processor (< 400 MHz), you will have to wait **several minutes** for the calculation of 200 excretion values to finish.

Tip: If your processor is **too slow**, **decrease** the number of **time points**.

D.3.13. Optimizing the Intake Estimates

This is done by improving the fit of the predicted bioassay quantity to the bioassay data - using the **Graph Tool** (Figure D.45):

- click the "**Select Axes Automatically**" button ("Tools" sub-panel);
- check the "**Plot**" dialog box under "**Bioassay Predictions**" ("Plot" sub-panel).

The **predicted values** of the **bioassay quantity** will automatically be added to the **graph of the data** (as a **green curve**).

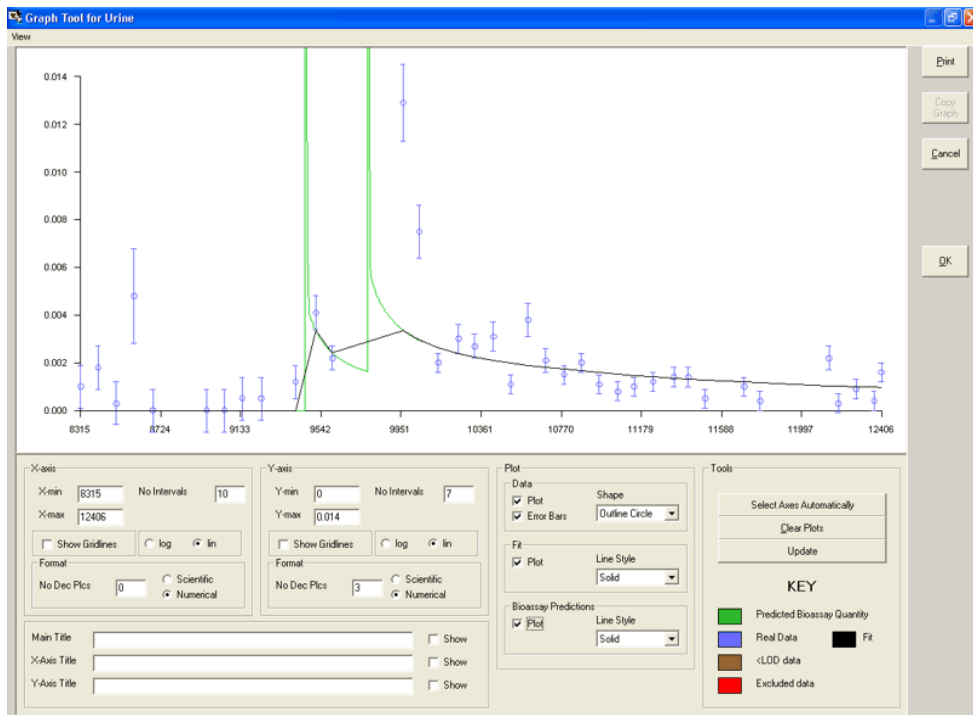


Figure D.45. Adding the "Bioassay Predictions" curve to the data plot.

The **predicted bioassay quantity** curve is also added automatically to the **Bioassay Quantity** window display (Figure D.46).

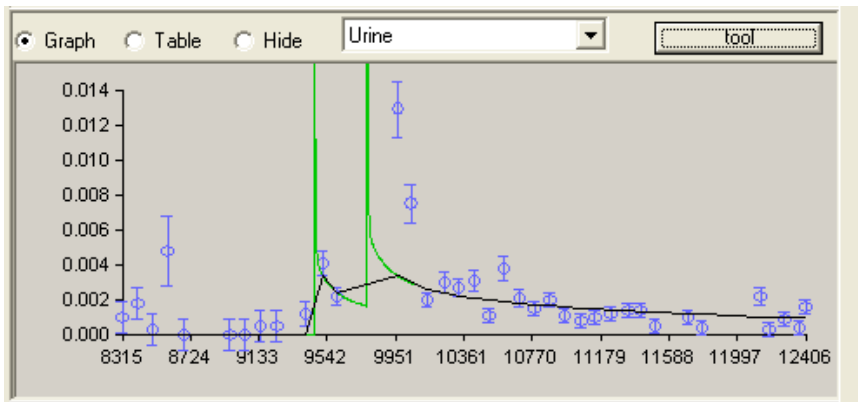


Figure D.46. Curve of predicted bioassay quantity displayed in **Bioassay Quantity** window.



Tip: Use the **higher resolution** provided by the **Graph Tool** for critical comparisons of predicted curves with the measured values.

Examine closely the **Graph Tool** plot (Figure D.45), and you will see that:

1. the **predicted** early urinary excretion for the **known** intake time (**IR2**) is substantially **higher** than the **next** measured value (at **9,516 d**);
2. the **next two data points** (at **9,516** and **9,601 d**) are **reasonably-well predicted**.
3. the values of the **two highest measured values** (following **IR3**) are **NOT predicted**.

Clearly, from the **predicted rapid fall-off** in urinary excretion, the **actual date of intake** for IR3 must have been much closer to **9/18/1972 (9,963 d)**, the date of the **next** urine sample, than the "mid-interval" date (**3/21/1972**) assumed initially for IR3.

To **test** this interpretation:

- in the **Main Screen**, *change* the assumed "**Start Date**" for IR3 to "**9/11/72**";
- back in the **Bioassay Calculations** screen, "**Bioassay to Intakes**" *option* (blue arrow), *click* the "**Start Calculation**" *button*.

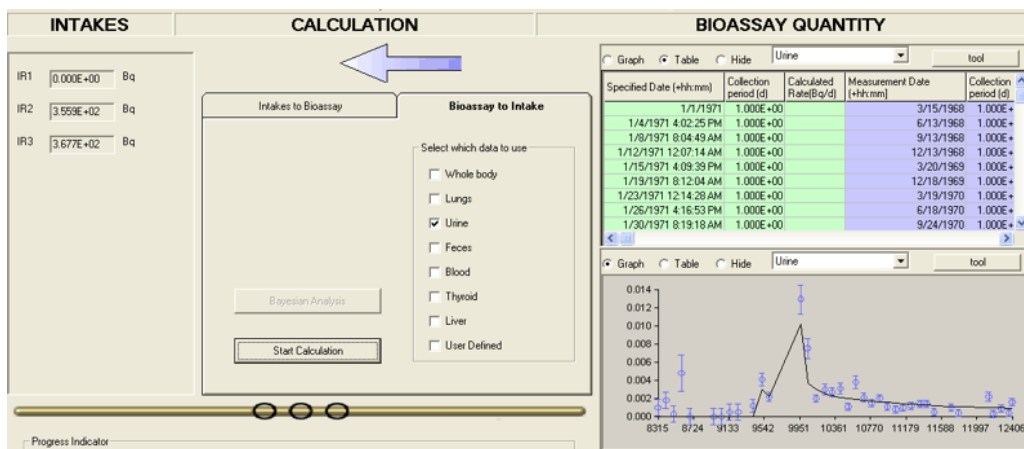


Figure D.47. Calculating new intake amounts for a different assumed date of intake for IR3.

With the **revised date of intake** for IR3, the calculated **Intakes** are:

- IR1 = 0 Bq;
- IR2 = 355.9 Bq;
- IR3 = 367.7 Bq.

Figure D.48 shows the enlarged plot in the **Graph Tool**.

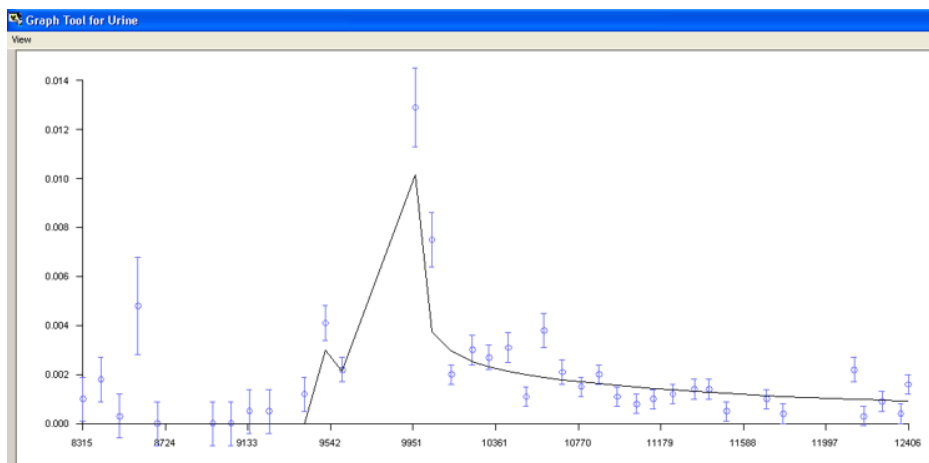


Figure D.48. Improved data fit obtained by refining the assumed date of intake for IR3.

To plot the corresponding **predicted** bioassay quantity **curve** simply:

- *switch* to the "**Intakes to Bioassay**" *option* (green arrow);
- *click* the "**Start Calculation**" *button*.

The **new predicted curve** will be displayed automatically in the **Bioassay Quantity** window. Open the **Graph Tool** (Figure D.49) to examine this.

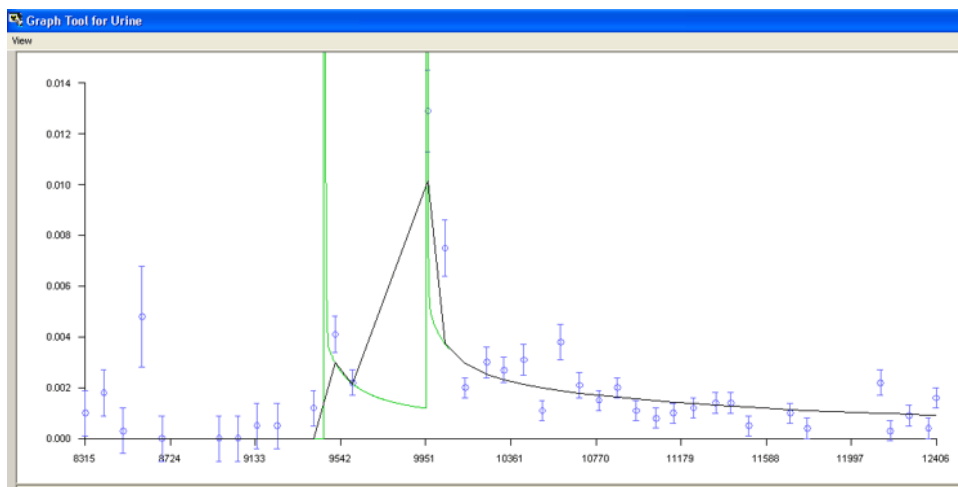


Figure D.49. Predicted rapid changes in urinary excretion from IR2 and IR3.

Comparison of the **predicted** (green curve) early urinary excretion following IR3 with the **measured** fall-off (between the samples at 9,963 d and 10,044 d) suggests that the **actual** fall-off in urinary excretion is substantially **slower** than **predicted** (by the assumed **Type M** absorption behavior). To test this interpretation, the assumed **absorption rate** for IR3 can be **changed**, and the **effect** on the fitted intake amounts and predicted urinary excretion curve can be *examined*, as follows:

- **Un-check "Apply Model Params to All IRs"** - in the **"Advanced"** menu (**Main Screen**). This will enable you to vary the absorption rate for IR3 independently of IR1 and IR2.
- **Increase the "Final dissolution rate, St"** for IR3 from $5 \times 10^{-3} \text{ d}^{-1}$ to $5 \times 10^{-2} \text{ d}^{-1}$.
- For consistency with an increased absorption rate, **decrease the aerosol AMAD to 0.5 μm** .
- Back in the **Bioassay Calculations** screen, **"Bioassay to Intakes"** option (blue arrow), click the **"Start Calculation"** button.

The result is shown in Figure D.50.

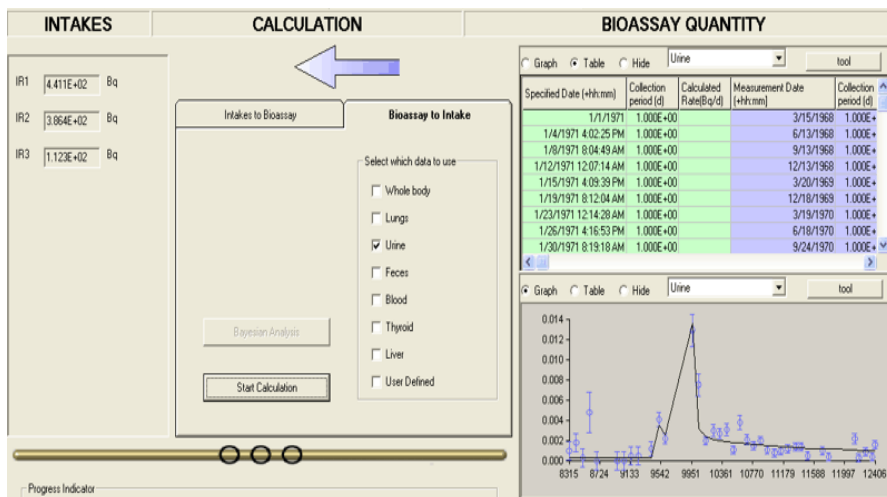


Figure D.50. Calculating new intake amounts for an increased absorption rate for IR3.



Note: Improving the data fit for IR3 enables the **maximum likelihood method** to fit simultaneously a **finite** intake amount for IR1.

With the **revised absorption rate** and **aerosol AMAD** for IR3, the calculated **Intakes** are:

- IR1 = 441.1 Bq;
- IR2 = 386.4 Bq;
- IR3 = 112.3 Bq.

Figure D.51 shows the enlarged plot in the **Graph Tool**.

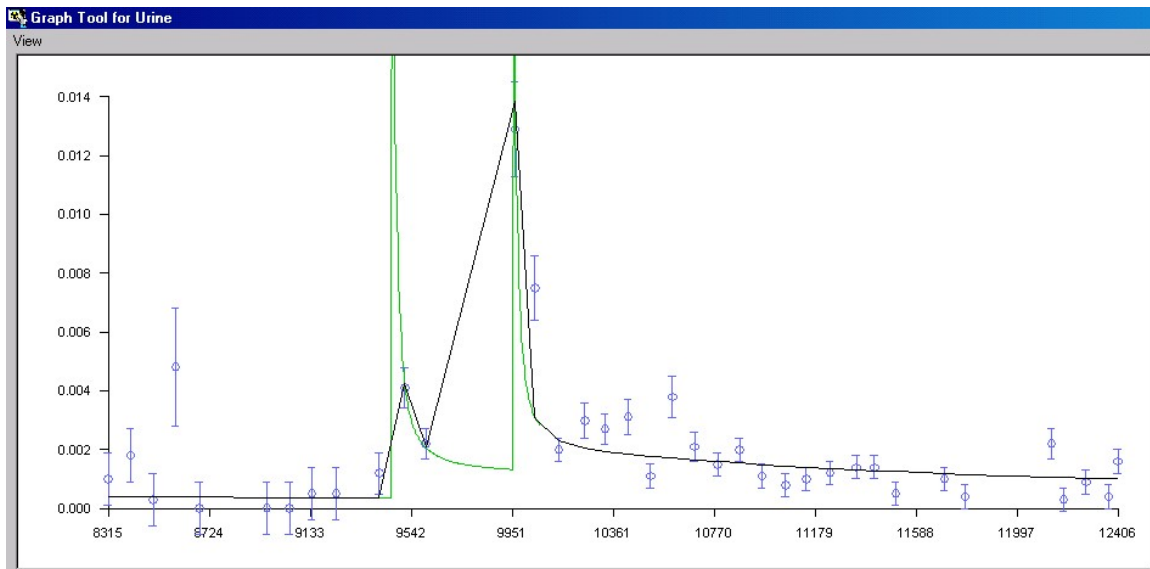
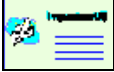


Figure D.51. Improved data fit by refining the assumed absorption rate and AMAD for IR3.



Warning: The "solution" of the *Miller et al. (1999)* case illustrated in Figure D.51 is NOT intended to be definitive - merely "illustrative" of the procedures available in **IMBA Expert™ OCAS/ORAU-Edition** for **estimating multiple intakes**. Inclusion of **additional information** about the nature of the three intakes considered here could well lead to a **different** set of estimates for the **intake amounts**.



Important: The decision on when the "parameter optimization" procedure has found an "acceptable" solution, will, of course, be determined by your Regulatory Guidance [e.g., for regulatory purposes in the U.S. by the *DOE Standard for Internal Dosimetry (DOE-STD-1121-98)*]. Your intake-fitting procedure should include the evaluation and consideration of the **resulting committed doses**. **IMBA Expert™ OCAS/ORAU-Edition** enables you to **evaluate these doses very easily** (by switching to the **Dose Calculations** screen) **after each stage** of the intake-fitting procedure.

D.4. Using Multiple Bioassay Quantities

This example is taken from *IAEA (1999)* - see Case #4 in their Appendix 2. A person (green activist) penetrated through barriers into an area of "low-level waste" in an abandoned sand mine. He found a barrel with a "radioactive substances" label, took out a tin labelled "**ISOMET ⁹⁰Sr**", opened the tin and found white powder. After a few days, the person started to "worry" - and sought out a measurement with a "dose-rate meter." This indicated serious external contamination. The high reading persisted after the person showered - indicating substantial internal contamination. Surface contamination was found in his home - and on various personal belongings.

The following bioassay monitoring was performed:

- **Whole body activity** - 15 measurements from approximately 5 days after the intake, over a 21-month period (see Table D.3).
- **Urine sampling** - 9 measurements from approximately 5 days after the intake, over a 9-month period (see Table D.4).
- **Fecal sampling** - 6 measurements from approximately 6 days after the intake, over a 10-day period (see Table D.5).

No "error" values were reported.

Table D.3. ⁹⁰Sr/⁹⁰Y whole body activity measurements.

Measurement date	Activity (kBq)	Measurement date	Activity (kBq)
November 29, 1990	692	December 12, 1990	215
November 30, 1990	400.5	May 27, 1991	118.5
December 3, 1990	292	June 5, 1991	135
December 4, 1990	272	July 4, 1991	110.5
December 5, 1990	256.5	August 8, 1991	102.5
December 6, 1990	261.5	June 2, 1992	96
December 7, 1990	248	August 11, 1992	79
December 10, 1990	218		

Table D.4. ⁹⁰Sr urine activity measurements.

Sample date	Collection period (h)	Daily excretion rate (kBq d ⁻¹)
November 29, 1990	19	56.60
December 1, 1990	-	55.28
December 3, 1990	19	14.46
December 4, 1990	19	10.81
December 6, 1990	18	9.80
December 9, 1990	19	5.91
December 11, 1990	24	4.44
July 3, 1991	24	0.47
August 7, 1991	24	0.20

Table D.5. ⁹⁰Sr fecal activity measurements.

Sample date	Collection period (h)	Daily excretion rate (kBq d ⁻¹)
December 1, 1990	-	8.54
December 3, 1990	-	2.56
December 4, 1990	-	10.52
December 6, 1990	-	0.36
December 9, 1990	-	0.12
December 11, 1990	-	2.3

No information was available on:

- the particle size of the powder;
- the chemical form of the powder;
- the nature of the intake (*i.e.*, whether by inhalation or ingestion).

This case can be solved (rapidly) with the following steps:

1. *assume* appropriate **errors**;
2. *assume* ICRP-recommended **bioassay models**;
3. *test* hypothetical **intake scenarios**;
4. *evaluate* the **likely intake**;
5. *evaluate* the **likely dose**.

D.4.1. Error Assumptions

No information on the magnitude of measurement errors is available in this example case. However, in order to give an appropriate "weight" to each set of bioassay measurements, it is important to assign a realistic error value for each type of data. Let's assume the following:

- **Whole body** activity measurements - **Relative** error with **K = 0.2** - **Normal** error distribution.
- **Urinary excretion rate** measurements - **Lognormal** error distribution - with $\sigma_g = 1.8$.
- **Fecal excretion rate** measurements - **Lognormal** error distribution - with $\sigma_g = 4.0$.



Note: These assumed errors are meant to reflect the fact that **Whole Body** measurements (of $^{90}\text{Sr}/^{90}\text{Y}$) are reasonably precise, whereas the **Urinary Excretion Rate** is subject to substantial biological variability, and the **Fecal Excretion Rate** to even greater biological variability.

The resulting tables of **input data**, completed in the **Table Tool**, are shown in Figures D.52 through D.54, for **Whole Body**, **Urine** and **Feces**, respectively.

Measurement Date [+hh:mm]	N/A	Measurement Value(Bq)	Data Type	Measurement Error	Error Distribution
11/29/1990 12:00:00 AM		6.92000E+05	Real	1.38400E+05	NORM
11/30/1990 12:00:00 AM		4.00500E+05	Real	8.0100E+04	NORM
12/3/1990 12:00:00 AM		2.92000E+05	Real	5.8400E+04	NORM
12/4/1990 12:00:00 AM		2.72000E+05	Real	5.4400E+04	NORM
12/5/1990 12:00:00 AM		2.56500E+05	Real	5.1300E+04	NORM
12/6/1990 12:00:00 AM		2.61500E+05	Real	5.2300E+04	NORM
12/7/1990 12:00:00 AM		2.48000E+05	Real	4.9600E+04	NORM
12/10/1990 12:00:00 AM		2.18000E+05	Real	4.3600E+04	NORM
12/12/1990 12:00:00 AM		2.15000E+05	Real	4.3000E+04	NORM
5/27/1991 12:00:00 AM		1.18500E+05	Real	2.3700E+04	NORM
6/5/1991 12:00:00 AM		1.35000E+05	Real	2.7000E+04	NORM
7/4/1991 12:00:00 AM		1.10500E+05	Real	2.2100E+04	NORM
8/8/1991 12:00:00 AM		1.02500E+05	Real	2.0500E+04	NORM
6/2/1992 12:00:00 AM		9.6000E+04	Real	1.9200E+04	NORM
8/11/1992 12:00:00 AM		7.9000E+04	Real	1.5800E+04	NORM

Figure D.52. Whole body data and assumed errors for IAEA Case #4.

Measurement Date (+hh:mm)	Collection period (d)	Measurement Rate(Bq/d)	Data Type	Measurement Error	Error Distribution
11/29/1990 12:00:00 AM	7.920E-01	5.6600E+04	Real	1.800E+00	LOGNORM
12/1/1990 12:00:00 AM	1.000E+00	5.5280E+04	Real	1.800E+00	LOGNORM
12/3/1990 12:00:00 AM	7.920E-01	1.4460E+04	Real	1.800E+00	LOGNORM
12/4/1990 12:00:00 AM	7.920E-01	1.0810E+04	Real	1.800E+00	LOGNORM
12/6/1990 12:00:00 AM	7.500E-01	9.800E+03	Real	1.800E+00	LOGNORM
12/9/1990 12:00:00 AM	7.920E-01	5.910E+03	Real	1.800E+00	LOGNORM
12/11/1990 12:00:00 AM	1.000E+00	4.440E+03	Real	1.800E+00	LOGNORM
7/3/1991 12:00:00 AM	1.000E+00	4.700E+02	Real	1.800E+00	LOGNORM
8/7/1991 12:00:00 AM	1.000E+00	2.000E+02	Real	1.800E+00	LOGNORM

Figure D.53. Urine data and assumed errors for IAEA Case #4.

Measurement Date (+hh:mm)	Collection period (d)	Measurement Rate(Bq/d)	Data Type	Measurement Error	Error Distribution
12/1/1990 12:00:00 AM	1.000E+00	8.540E+03	Real	4.000E+00	LOGNORM
12/3/1990 12:00:00 AM	1.000E+00	2.560E+03	Real	4.000E+00	LOGNORM
12/4/1990 12:00:00 AM	1.000E+00	1.0520E+04	Real	4.000E+00	LOGNORM
12/6/1990 12:00:00 AM	1.000E+00	3.600E+02	Real	4.000E+00	LOGNORM
12/9/1990 12:00:00 AM	1.000E+00	1.200E+02	Real	4.000E+00	LOGNORM
12/11/1990 12:00:00 AM	1.000E+00	2.300E+03	Real	4.000E+00	LOGNORM

Figure D.54. Fecal data and assumed errors for IAEA Case #4.

D.4.2. Select Reference Bioassay Models

Once you have defined the **Indicator Nuclide** (^{90}Sr), and also the **Bioassay Quantities** (in the **Bioassay Quantity** windows), you can specify use of ICRP's currently recommended **Bioassay Models** in one quick step - by clicking the "ICRP DEFS Load" icon (Figure D.55).

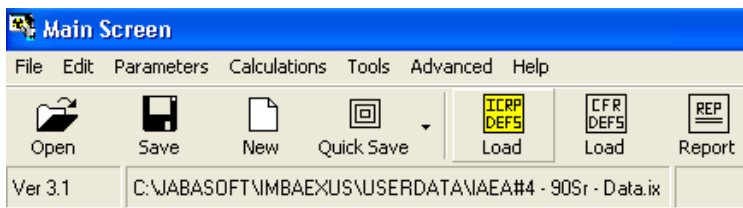


Figure D.55. The "ICRP DEFS Load" icon for specifying use of all ICRP default models.

You will be prompted to select an "**f1 Value**" and "**Absorption Type**" for the ^{90}Sr material (Figure D.56). Select type "M".

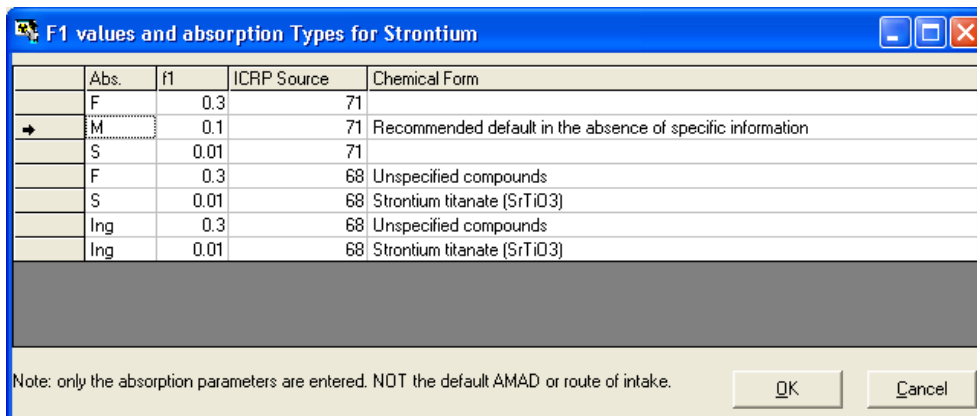


Figure D.56. Selecting the f1 value and absorption type for **Strontium**.

If you then *click* the "**Bioassay**" button in the "**Model Parameters**" panel (**Main Screen**) you will see that the "**Std Sr Model**" bioassay models have been *loaded* for **Whole body**, **Urine** and **Feces** (Figure D.57).

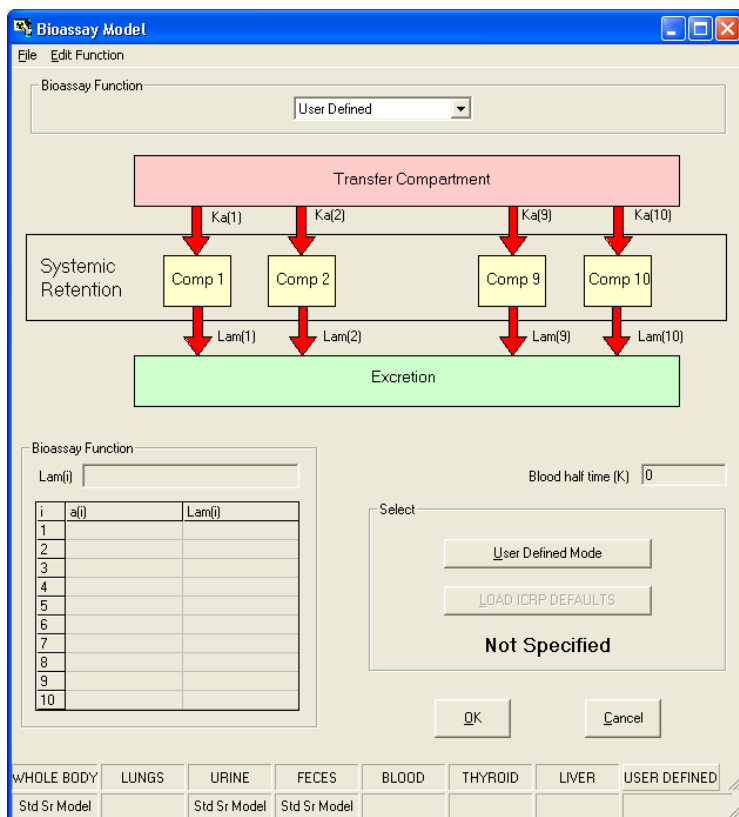


Figure D.57. Confirming that the "**Std Sr Model**" has been loaded for **Whole Body**, **Urine** and **Feces**.

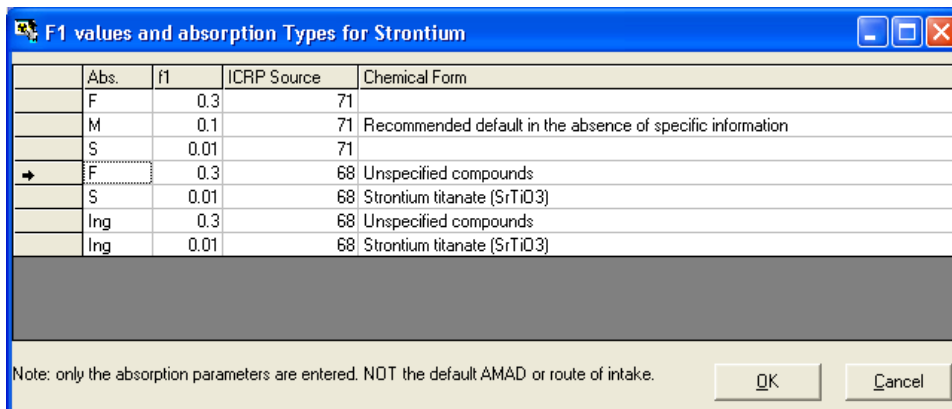
D.4.3. Hypothetical Intake Scenarios

The nature of the intake was unknown in this case (IAEA Case #4) - so let's try to get **IMBA Expert™ OCAS/ORAU-Edition** to indicate the most likely type of intake! To do this we simply have to set up several hypothetical intake scenarios to occur simultaneously - and let **IMBA Expert™ OCAS/ORAU-Edition** use the bioassay data (whole body, urine and feces) simultaneously to "choose" the most likely scenario.

Important Note: The availability of **3 independent sets of bioassay data** - plus the ability to analyse these data **simultaneously** - makes it possible to apply **IMBA Expert™ OCAS/ORAU-Edition** in this manner to determine the relative "weight" of several hypothetical intake scenarios - when the actual conditions of intake are unknown. This method is **not likely to work** if you have data on just **one bioassay quantity**!

In this example case, we don't know whether the intake occurred by **inhalation** or **ingestion**, or by a **combination of both**. We also know nothing about the **chemical form** of the material, or

the **particle size distribution of any airborne material**. ICRP's recommendations concerning potential chemical forms of **strontium** are displayed in the "**F1 values and absorption Types for Strontium**" window (Figure D.58).



Abs.	f1	ICRP Source	Chemical Form
F	0.3	71	
M	0.1	71	Recommended default in the absence of specific information
S	0.01	71	
→ F	0.3	68	Unspecified compounds
S	0.01	68	Strontium titanate (SrTiO3)
Ing	0.3	68	Unspecified compounds
Ing	0.01	68	Strontium titanate (SrTiO3)

Note: only the absorption parameters are entered. NOT the default AMAD or route of intake.

OK Cancel

Figure D.58. ICRP's currently recommended "**default**" values for **Strontium** gut uptake fraction and absorption Type.

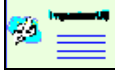
Let's try setting up **4** hypothetical (but possible) intake scenarios, and seeing if **IMBA Expert™ OCAS/ORAU-Edition** can distinguish between them, as follows:

- **IR1** - Ingestion - with $f_1 = 0.1$.
- **IR2** - Inhalation - ICRP default aerosol - Type "F" absorption ($f_1 = 0.3$).
- **IR3** - Inhalation - ICRP default aerosol - Type "M" absorption ($f_1 = 0.1$).
- **IR4** - Inhalation - ICRP default aerosol - Type "S" absorption ($f_1 = 0.01$).

To do this (most easily):

- *select 4 Intake Regimes;*
- *click "ICRP DEFS Load";*
- *un-check "Apply Model Parameters to All IRs" - in the "Advanced" menu;*
- *set each IR in turn, as listed above.*

Figure D.59 shows the resulting **Main Screen** set to indicate the **Model Parameters** for **IR1** (the hypothetical **Ingestion**).



Note: In this case, the actual intake probably occurred on **November 24th, 1990** - about five days before the first whole body count and urine sample. The "**Start Date**" for each hypothetical (acute) intake is therefore set to "**11/24/90**".

Intake Scenario

Intake Regimes: Enter Number of Intake Regimes (1-10): 4

IR 1 | IR 2 | IR 3 | IR 4

Route: ☐ Inhalation ☒ Ingestion ☐ Injection ☐ Wound ☐ Vapor

Mode: ☒ Acute ☐ Chronic

Start Date: 11/24/1990

Units: Specify Time As: ☒ Date ☐ Time (d)

Intake: ☒ Bq ☐ dpm ☐ pCi ☐ mg

Dose: ☒ Sv ☐ rem ☐ mSv ☐ mrem

Indicator Nuclide: Select Radionuclide: **Sr-90**

Number of Associated Radionuclides: 0

Half Life: 1.063E+04 d

Associated Radionuclides: None Selected

Model Parameters

IR1 | IR2 | IR3 | IR4

Respiratory Tract: Deposition, Vapor, Wound, Bioassay, Particle Transport, Absorption, GI-Tract, Biokinetics

OCAS
Office of Compensation
Analysis and Support

Calculations

Bioassay Calculations
Dose Calculations

IR 1 | Absorption: Type F | Part Tran: ICRP Defaults | GI-Tract: ICRP Defaults | f1=0.1 | Biokinetics: ICRP SI Model | Deposition: User Defined | N/A | Wound: Not Specified

Figure D.59. First hypothetical intake regime (IR1) set up as "Ingestion" with $f_1 = 0.1$.

To calculate the most likely amounts of intake from each IR (in the **Bioassay Calculations Screen**):

- check **Whole body, Urine** and **Feces** (in the **Bioassay to Intake** mode);
- click "**Start Calculation**".

Figure D.60 shows the result.

Bioassay Calculations

INTAKES

IR1: 5.279E+06 Bq
IR2: 5.616E+05 Bq
IR3: 5.503E+04 Bq
IR4: 4.076E-01 Bq

CALCULATION

Intakes to Bioassay
Bioassay to Intake

Select which data to use:

☒ Whole body
☐ Lungs
☐ Urine
☒ Feces
☐ Blood
☐ Thyroid
☐ Liver
☐ User Defined

Progress Indicator

Deposition: [Progress Bar]
Collating Times: [Progress Bar]
Bioassay Calcs: [Progress Bar]
Current Operation: [Progress Bar]

Calculation Complete

BIOASSAY QUANTITY

Whole body

Measurement Date (yymmdd)	Measurement Value(Bq)	Data Type	Measurement Error	Error Distribution
11/29/1990	1.52000E+05	Real	1.36400E+05	NORM
11/30/1990	1.00500E+05	Real	8.0100E+04	NORM
12/3/1990	1.20000E+05	Real	5.8400E+04	NORM
12/4/1990	2.72000E+05	Real	5.4400E+04	NORM
12/5/1990	1.56500E+05	Real	5.1300E+04	NORM
12/6/1990	1.61500E+05	Real	5.2300E+04	NORM
12/7/1990	1.48000E+05	Real	4.9600E+04	NORM
12/10/1990	2.18000E+05	Real	4.3600E+04	NORM
12/12/1990	2.15000E+05	Real	4.3000E+04	NORM

Urine

Measurement Date (yymmdd)	Collection period (d)	Measurement Rate(Bq/d)	Data Type	Measurement Error	Error Distribution
11/29/1990	7.500E-01	5.6600E+04	Real	1.800E+00	LOGNORM
12/1/1990	1.000E+00	5.5200E+04	Real	1.800E+00	LOGNORM
12/3/1990	7.500E-01	1.4460E+04	Real	1.800E+00	LOGNORM
12/4/1990	7.500E-01	1.0810E+04	Real	1.800E+00	LOGNORM
12/6/1990	7.500E-01	9.800E+03	Real	1.800E+00	LOGNORM
12/9/1990	7.500E-01	5.910E+03	Real	1.800E+00	LOGNORM
12/11/1990	1.000E+00	4.440E+03	Real	1.800E+00	LOGNORM
7/3/1991	1.000E+00	4.700E+02	Real	1.800E+00	LOGNORM
8/7/1991	1.000E+00	2.000E+02	Real	1.800E+00	LOGNORM

Feces

Measurement Date (yymmdd)	Collection period (d)	Measurement Rate(Bq/d)	Data Type	Measurement Error	Error Distribution
12/1/1990	1.000E+00	8.540E+03	Real	4.000E+00	LOGNORM
12/3/1990	1.000E+00	2.560E+03	Real	4.000E+00	LOGNORM
12/4/1990	1.000E+00	1.0520E+04	Real	4.000E+00	LOGNORM
12/6/1990	1.000E+00	3.600E+02	Real	4.000E+00	LOGNORM
12/9/1990	1.000E+00	1.200E+02	Real	4.000E+00	LOGNORM
12/11/1990	1.000E+00	2.300E+03	Real	4.000E+00	LOGNORM

OK

Sr-90 | Max Likelihood fit

Figure D.60. Calculated amounts of 4 hypothetical intakes.

The resulting **total** estimated intake is about **5.92 MBq**, of which:

- **IR1** is assigned about **89%**;
- **IR2** is assigned about **10%**;
- **IR3** is assigned about **1%**;
- **IR4** is assigned **0.001%**.

Figure D.61 shows the resulting overall "fits" to all 3 sets of bioassay data.

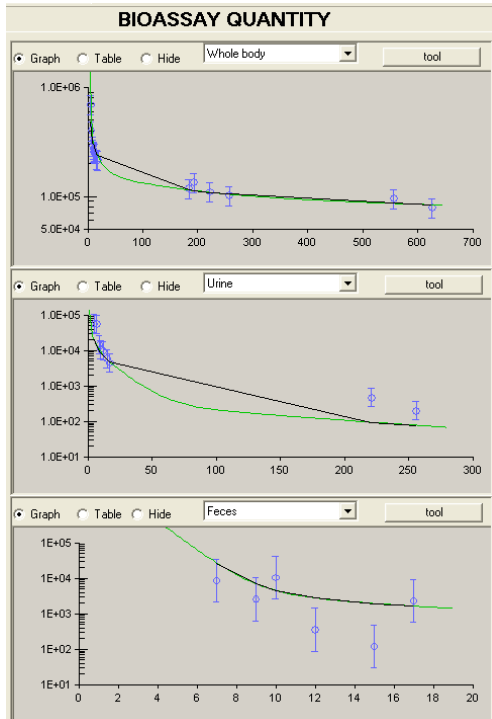


Figure D.61. Overall fits to the bioassay data given by a combination of 4 hypothetical acute intakes.

From the above, we can conclude that:

- the overall fits to all 3 sets of bioassay data are reasonably consistent with the assumed error distributions;
- inhalation intake of both Types "S" and "M" material can be neglected in comparison with that of Type "F" - and that by ingestion.

We now need to refine our hypothetical intake scenario(s) accordingly (see the next section).

D.4.4. Refining the Intake Assessment

From the initial evaluation of hypothetical intake scenarios, it was clear that the actual intake comprised primarily of:

- ingestion, and/or;
- inhalation of Type "F" material.

In this case, we can proceed to test hypothetical combinations of ingestion (with $f_1 = 0.3$) and inhalation (Type "F" with various assumed values of the AMAD), as follows:

- **IR1** - Ingestion - with $f_1 = 0.3$.
- **IR2** - Inhalation - Type "F" absorption - with AMAD = 5 μm (ICRP default aerosol);
- **IR3** - Inhalation - Type "F" absorption - with AMAD = 20 μm ;
- **IR4** - Inhalation - Type "F" absorption - with AMAD = 100 μm .

Figure D.62 shows the result.

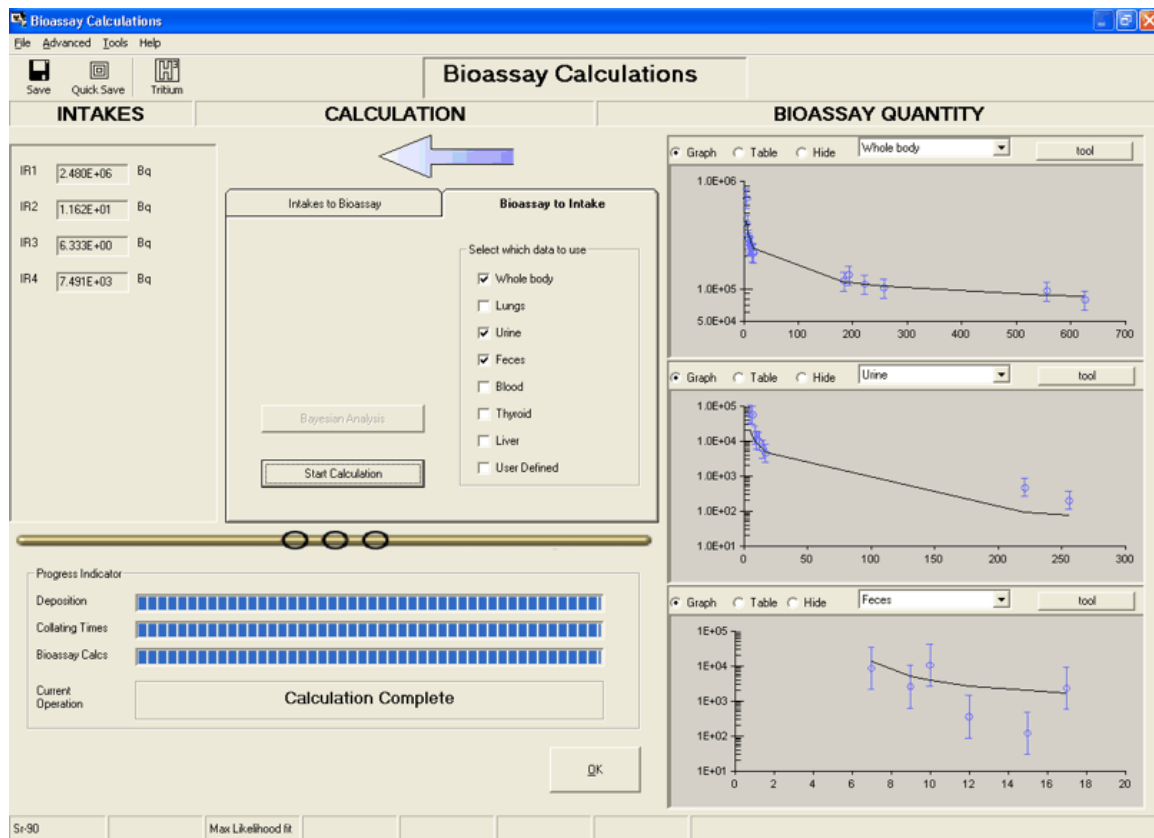


Figure D.62. Intake amounts calculated for 4 hypothetical (simultaneous) intake scenarios.

The "best estimates" of each type of intake are:

- **IR1** - Ingestion - **2.480 MBq**;
- **IR2** - Inhalation - 5 μm AMAD - **11.62 Bq**;
- **IR3** - Inhalation - 20 μm AMAD - **6.333 Bq**;
- **IR4** - Inhalation - 100 μm AMAD - **7.491 kBq**.

Clearly, the bioassay data (in conjunction with ICRP's current respiratory tract model and biokinetic model for strontium) indicate intake predominantly by ingestion. Figures D.63 through D.65 show the fits obtained, for the whole body, urine and fecal data, respectively.

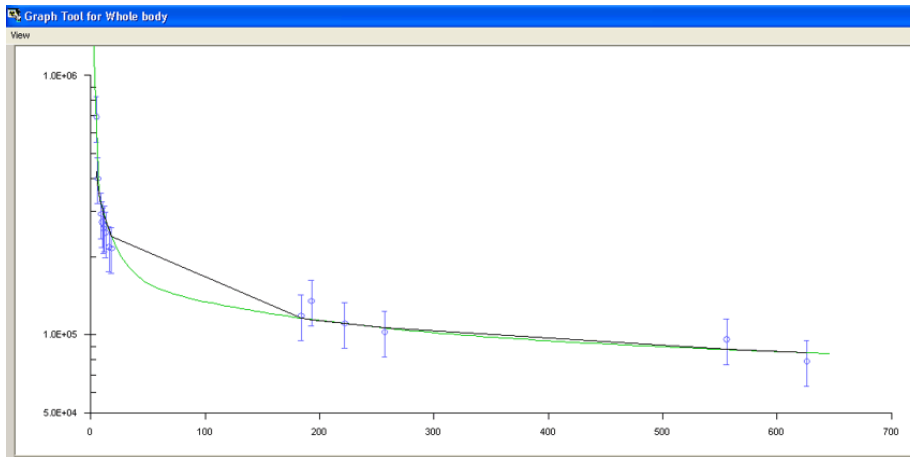


Figure D.63. Graph Tool plot of whole body data.

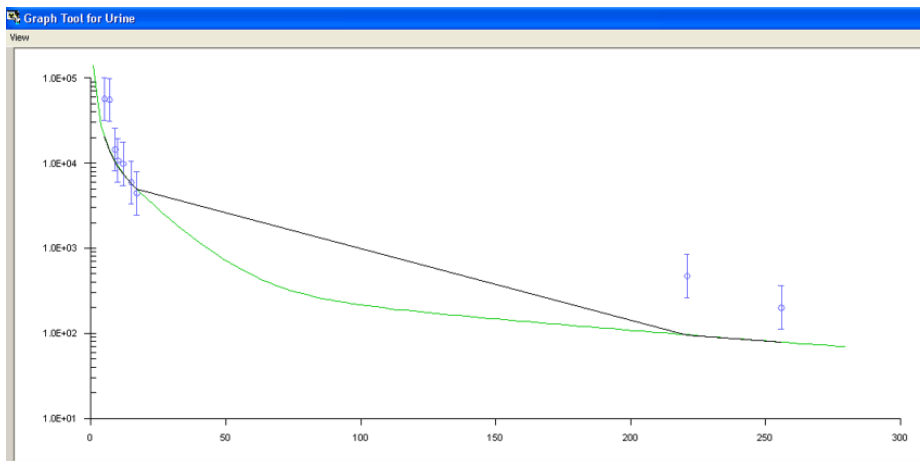


Figure D.64. Graph Tool plot of urine data.

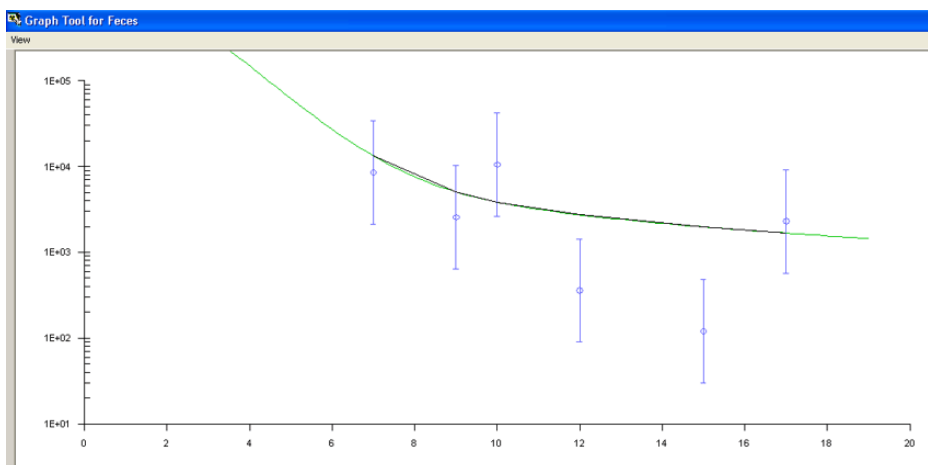


Figure D.65. Graph Tool plot of fecal data.

Except for the additional retention in the nose and tracheobronchial region, inhalation of very large particles has a similar effect to ingesting these particles - since most of the inhaled activity not cleared from the nares (by nose blowing) is swallowed. If we had assumed that ALL of the

intake had occurred by inhalation of a 100- μm -AMAD aerosol, the resulting "fit" to the bioassay data would have been as shown in Figure D.66. In this case, the estimated intake would have been **4.438 MBq**.

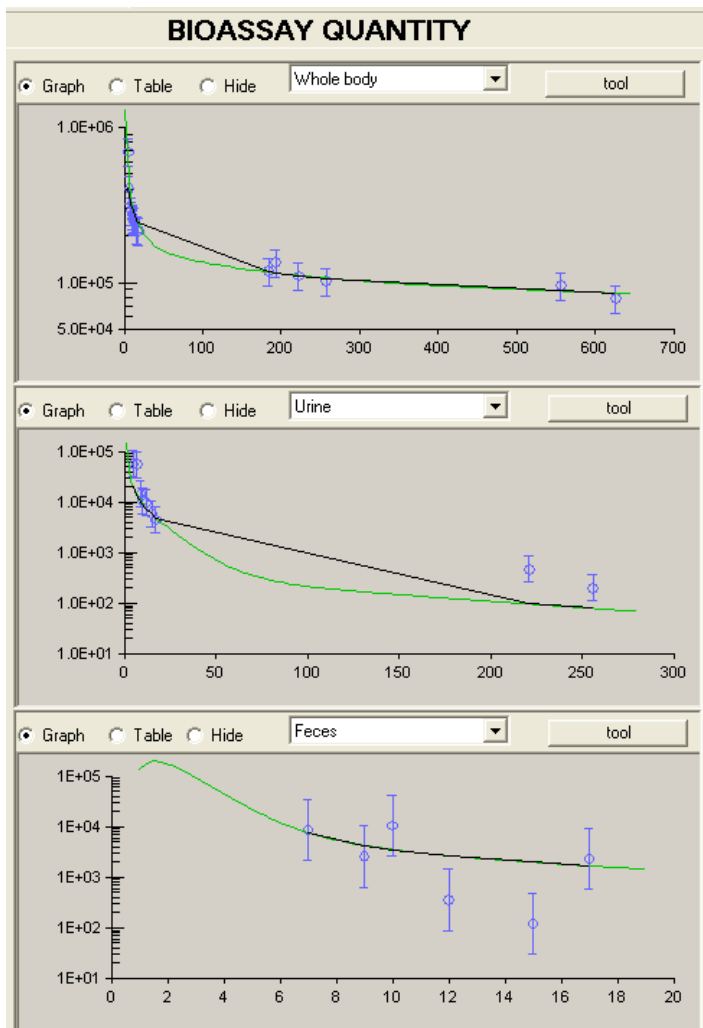


Figure D.66. "Best Fit" to the bioassay data obtained when the intake is assumed to be by ingestion.

By eye, it is impossible to distinguish between the "fit" shown in Figure D.66 (assuming intake by inhalation of large particles) from that shown in Figure D.62 (assuming predominant intake by ingestion). However, in terms of "numerical likelihood," **IMBA Expert™ OCAS/ORAU-Edition** found the fit in Figure D.62 (ingestion) substantially "better." However, for radiological protection purposes, it is prudent to consider which intake route would give the higher effective dose - see the next section.



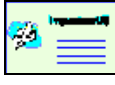
Tip: **IMBA Expert™ OCAS/ORAU-Edition** is designed to make it easy for you to test a range of hypothetical intake scenarios - when knowledge of the conditions of intake is sparse (as is often the case). It is then just as easy (and quick) to examine the implications of the most likely scenarios for dose.

D.4.5. Evaluating the Dose

As the final step in this example, we will calculate the doses resulting from the two "hypothetical" intake scenarios that we found to be most consistent with the bioassay data:

1. Ingestion of 2.486 MBq of material with an f_1 of 0.3.
2. Inhalation of 4.438 MBq of a 100- μm -AMAD aerosol of Type "F" material.

Figures D.67 and D.68, respectively, give the resulting values of effective dose.



Note: The **Associated Radionuclide** (^{90}Y) is included in the dose calculations. The ICRP-recommended biokinetic models are assumed for both ^{90}Sr and ^{90}Y , and also the ICRP68 radiation and tissue weighting factors.

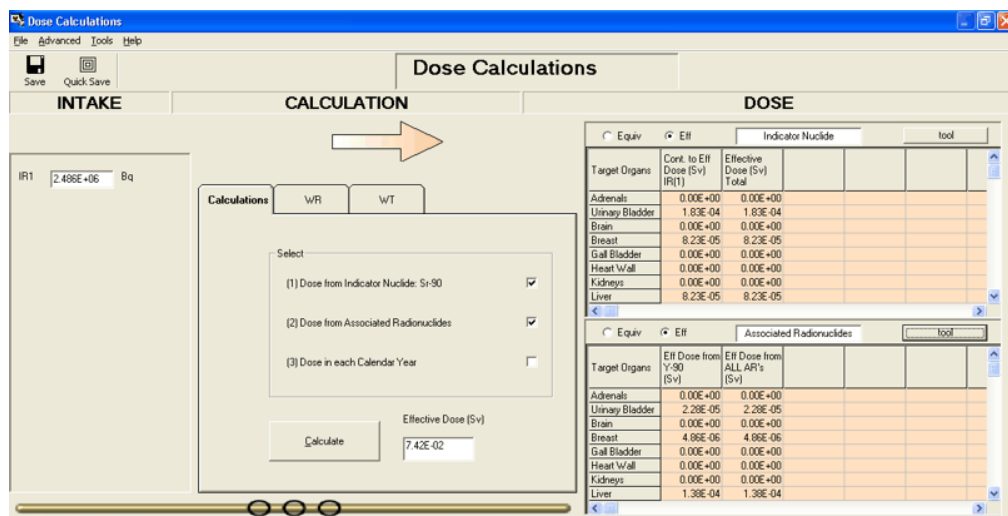


Figure D.67. Effective doses calculated for ingestion of $^{90}\text{Sr}/^{90}\text{Y}$ powder.

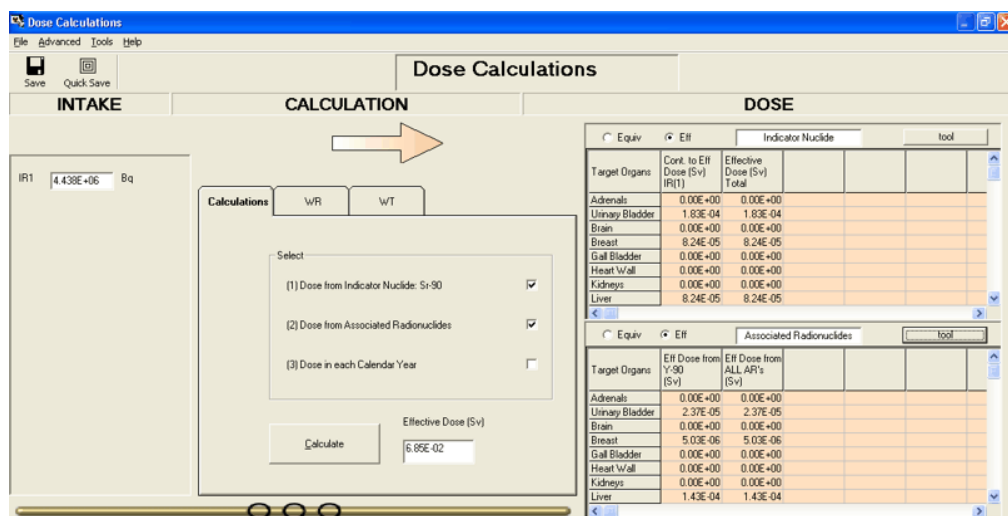


Figure D.68. Effective doses calculated for inhalation of $^{90}\text{Sr}/^{90}\text{Y}$ aerosol (100- μm -AMAD, Type "F").

Table D.6. Comparison of effective doses calculated by assuming intake by ingestion or inhalation.

Route of Intake	Effective Dose from ^{90}Sr (mSv)	Effective Dose from ^{90}Y (mSv)	Total Effective Dose (mSv)
Ingestion	68.6	5.64	74.2
Inhalation	66.5	1.96	68.5

Clearly, in this case, we can conclude that:

- the total effective dose is about **75 mSv**;
- it makes little difference if the actual intake occurred by ingestion or inhalation.



Note: The **Associated Radionuclide** (^{90}Y) is included in the dose calculations. The ICRP-recommended biokinetic models are assumed for both ^{90}Sr and ^{90}Y , and also the ICRP68 radiation and tissue weighting factors.

D.5. Uranium Isotopic Mixture

The case information was as follows:

- A release of uranium feed material at a uranium fuel fabrication plant was indicated by an installed continuous air monitor.
- The material released was sintered LEU of known isotopic composition, in the form of highly insoluble oxide.
- Earlier studies of airborne contamination in this area of the workplace indicated an aerosol AMAD of 5.9 μm .
- Both urine and fecal bioassay was carried out for the worker concerned, commencing immediately.

The isotopic composition of the uranium mixture (by activity) was:

- ^{234}U - 83.6%.
- ^{235}U - 3.05%.
- ^{238}U - 13.4%.

The following urine bioassay data were available:

- The first urine sample was obtained from the worker concerned at 30 minutes after the incident.
- Ten further (contiguous) samples were collected over the following 3 days.
- The results were reported as total uranium **mass (μg)** per collection period, together with the associated uncertainty (measurement error) and the total volume of urine collected.

The following fecal bioassay data were available:

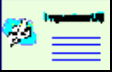
- The first fecal sample was obtained from the worker concerned at 3 hours after the incident.
- Four further (contiguous) samples were collected over the following 3 days.

- The results were reported as total uranium **activity (pCi)** per collection period, together with the associated uncertainty (measurement error).

Steps in Case Analysis

Follow these steps to analyze this case:

- Set up Uranium Mixture.
- Enter Uranium-in-Urine Data (in mg/d).
- Enter Uranium-in-Feces Data (in mg/d).
- Initial Joint Analysis of Urine/Fecal Data.
- Correct for Dietary Uranium Intake.
- Optimize Intake Model Parameters.
- Calculate Committed Doses.



Note: This case demonstrates how to use **IMBA Expert™ OCAS/ORAU-Edition** to detect the (assumed) constant background contributions to urinary and fecal excretion rates made by an individual's dietary intake of uranium.

D.5.1. Set Up Uranium Mixture

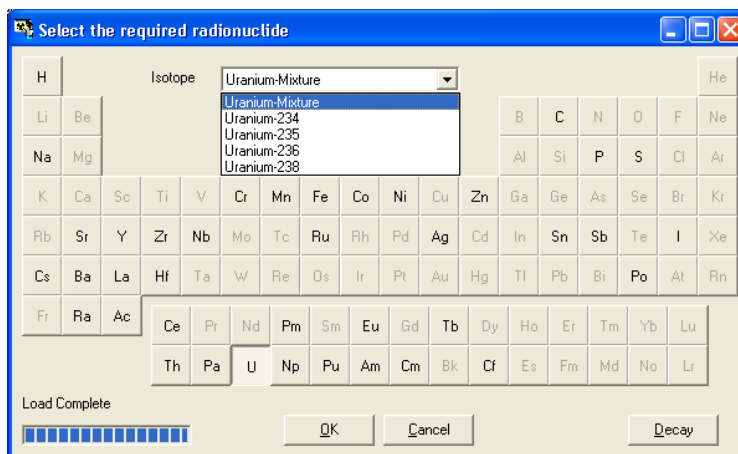


Figure D.69. Selecting **Uranium-Mixture** as the Indicator Nuclide.

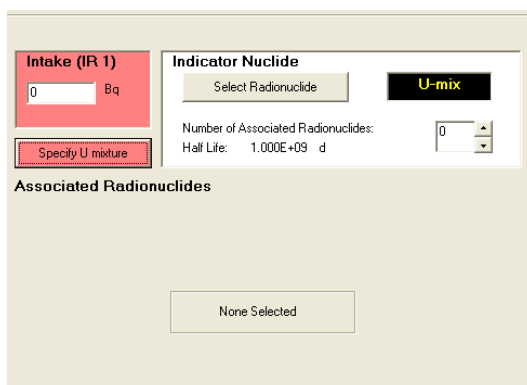


Figure D.70. "Specify U mixture" button.

Details of uranium mixture

Help

Isotopic Abundance

Isotope	Abundance (%)
U-234	83.6
U-235	3.05
U-236	0
U-238	13.4

Select

- ☒ User Defined
- ☐ Depleted
- ☐ Natural
- ☐ Low-Enriched
- ☐ High Enriched

Select by

- ☒ Activity
- ☐ Mass

Clear

Resulting Specific Activity

Unit	Value
Bq/mg	8.9611E+01
pCi/mg	2.4219E+03

Allow Units

- ☒ mg

OK Cancel

Figure D.71. User Defined details of uranium mixture with resulting specific activity.

Warning

Abundances do not add up to 100%
Do you still wish to leave this form?

Yes No

Figure D.72. Warning notice.

Units

Specify Time As

- ☐ Date
- ☒ Time (d)

since

1/1/1980 #

Intake

- ☐ Bq
- ☐ dpm
- ☐ pCi
- ☒ mg

Dose

- ☐ Sv
- ☐ rem
- ☐ mSv
- ☒ mrem

Intake (IR 1)

0 mg

Specify U mixture

Indicator Nuclide

Select Radionuclide

U-mix

Number of Associated Radionuclides: 4

Half Life: 1.000E+09 d

Associated Radionuclides

Radionuclide	Abundance (%)	Half Life (d)
U-234	83.6	8.924E+07
U-235		
U-236		
U-238		

Select Radionuclide

Delete Radionuclide

Figure D.73. Selected U-mix showing **Associated Radionuclides** and "mg" Intake Unit.

To define the **isotopic composition** and **measurement unit** for the uranium mixture:

1. Select "**Uranium-Mixture**" as the **Indicator Nuclide** (Figure D.69).
2. Click the "**Specify U mixture**" button (Figure D.70).

3. Enter the **Isotopic Abundance** values (% by **Activity** in this case), check the **Allow Units "mg"** box (Figure D.71), and click "OK".
4. You will be **warned** if your **Abundance** values don't add up to 100% (Figure D.72) - ignore the warning for this example.
5. Select **"mg"** in the **"Units"** panel (Figure D.73) - since, in this example, most of the measurements (urinary excretion rates) are reported in **"mg/d"**.

Note #1: The calculated specific activity of the defined uranium mixture is automatically displayed in the "details of uranium mixture" window" (Figure D.71).

Note #2: The individual uranium isotopes (^{234}U , ^{235}U , ^{236}U and ^{238}U) are automatically loaded as **Associated Radionuclides**. This is done in readiness for the **Dose Calculation**.

D.5.2. Enter Uranium-in-Urine Data (in mg/d)

Figure D.74 shows the urine bioassay data as entered in a NotePad® text file, ready for importing into the **Table Tool** of **IMBA Expert™ OCAS/ORAU-Edition**. **Note that:**

- These are *real* data.
- The dates have been changed (by subtracting from the reported values a constant number of yy:mm:hh) - in order to preserve confidentiality.
- The third column of values (the actual *bioassay quantity*) is the calculated daily uranium excretion rate - in $\mu\text{g d}^{-1}$.
- We have assumed a *lognormal* error distribution, with a σ_g of **1.8**. This is a more realistic representation of the data variability than the reported *measurement* uncertainties. The measurement uncertainties do NOT represent the sytematic (biological) variability in urinary excretion - which is substantially greater.

3/10/1995 12:30:00 AM	2.080E-02	1.830E-02	Real	1.8	LOGNORM
3/10/1995 5:30:00 AM	2.080E-01	5.640E-04	Real	1.8	LOGNORM
3/10/1995 12:15:00 PM	2.810E-01	3.770E-04	Real	1.8	LOGNORM
3/10/1995 11:05:00 PM	4.510E-01	1.510E-04	Real	1.8	LOGNORM
3/11/1995 6:10:00 AM	2.950E-01	1.380E-04	Real	1.8	LOGNORM
3/11/1995 4:20:00 PM	4.240E-01	1.070E-04	Real	1.8	LOGNORM
3/11/1995 4:30:00 PM	6.940E-03	2.620E-03	Real	1.8	LOGNORM
3/11/1995 8:50:00 PM	1.670E-01	2.180E-04	Real	1.8	LOGNORM
3/11/1995 10:50:00 PM	8.330E-02	3.430E-04	Real	1.8	LOGNORM
3/12/1995 2:30:00 AM	1.670E-01	2.180E-04	Real	1.8	LOGNORM
3/12/1995 4:30:00 PM	5.830E-01	7.890E-05	Real	1.8	LOGNORM

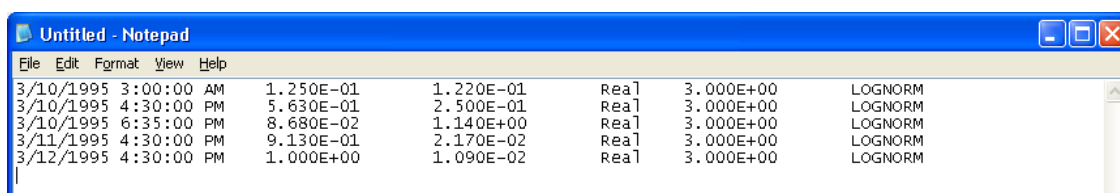
Figure D.74. Uranium-in-urine bioassay data set.

Tip: The reported (normal) measurement errors are given in the data file **"IU_URINE_2.txt"** - which is included in the **[Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo** folder at installation. It is instructive to re-analyze this case using these reported errors instead of the (realistic) *lognormal* errors.

D.5.3. Enter Uranium-in-Feces Data (in mg/d)

Figure D.75 shows the fecal bioassay data as entered in a NotePad® text file, ready for importing into the **Table Tool** of **IMBA Expert™ OCAS/ORAU-Edition**. **Note that:**

- Again, these are *real* data.
- Again, the dates have been changed (by subtracting from the reported values the same number of yy:mm:hh as for the urine data) - in order to preserve confidentiality.
- The third column of values (the actual *bioassay quantity*) is the calculated daily uranium excretion rate - in $\mu\text{g d}^{-1}$. These values are calculated from the reported values of excretion rate in terms of pCi d^{-1} , using the displayed (calculated) **specific activity** of the mixture (**2,421.9 pCi/mg** - see Figure D.71).
- We have assumed a *lognormal* error distribution, with a σ_g of **3.0**, c.f., $\sigma_g = 1.8$ for the urine data. This is a more realistic representation of the variability in fecal excretion rate than the reported *measurement* uncertainties. The raw measurement uncertainties drastically underestimate the systematic (biological) variability in fecal excretion.



Date/Time	Activity	Rate	Error Distribution
3/10/1995 3:00:00 AM	1.250E-01	1.220E-01	Real
3/10/1995 4:30:00 PM	5.630E-01	2.500E-01	Real
3/10/1995 6:35:00 PM	8.680E-02	1.140E+00	Real
3/11/1995 4:30:00 PM	9.130E-01	2.170E-02	Real
3/12/1995 4:30:00 PM	1.000E+00	1.090E-02	Real

Figure D.75. Uranium-in-feces bioassay data set.



Tip: The reported (normal) measurement errors are given in the data file "IU_FECES_2.txt" - which is included in the [Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo\ folder at installation. It is instructive to re-analyze this case using these reported errors instead of the (realistic) *lognormal* errors.

D.5.4. Initial Joint Analysis of Urine/Fecal Data

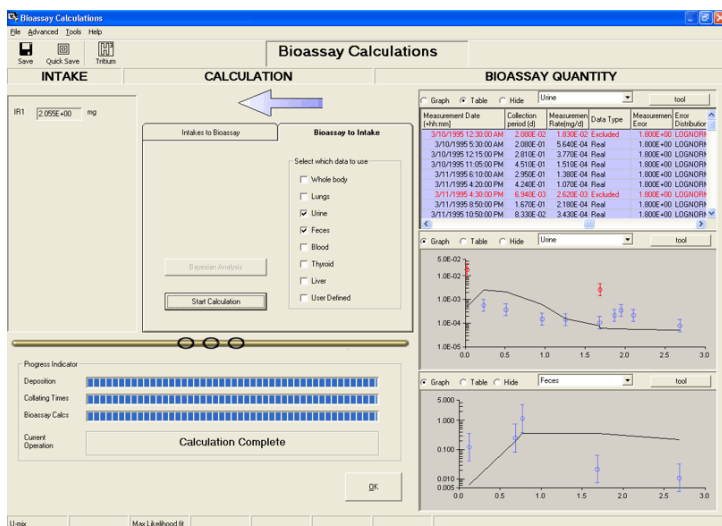


Figure D.76. Initial data "fit" for assumed acute inhalation of Type 'S' uranium at t = 0.

Figure D.76 shows the initial result of analysing jointly the measured urinary and fecal excretion rates, under the following assumptions:

- **Acute inhalation**, at $t = 0$.
- **Aerosol characteristics** - $AMAD/MMAD = 5.9 \mu\text{m}$, $\sigma_g = 2.5$, particle density (ρ) = 10 g cm^{-3} , particle shape factor (SF) = 1.5.
- **Absorption characteristics** - Type 'S'.
- **Mechanical transport parameters** (respiratory tract) - **ICRP66 Default**.
- **GI-Tract transport parameters** - **ICRP66 Default**.
- **Gut uptake fraction** (f_1) - 0.002 (**ICRP68** - highly insoluble uranium compounds: UO_2 , U_3O_8).
- Two **reported** uranium-in-urine **outlier values** have been **excluded** from the "fit":
 - the *first value* (from the sample collected 30 minutes after the intake) is assumed to result from *sample contamination*. the rate of excretion of uranium in urine following an acute intake requires several hours to "**build up**" - it does NOT *decrease* over this period.
 - the *seventh value* (from the sample collected at about 1.8 d after the intake) is also assumed to result from *sample contamination*.

Initial findings from plotted data fits

The resulting initial data fits (Figure D.76) show clearly that:

- After peaking at about 0.2 day after the intake, the *predicted* urinary excretion rate *falls off more rapidly* than the measured values.
- After the first day, the observed urinary excretion rates are *relatively constant*.
- The predicted fecal excretion rate *peaks at approximately the same time* after intake as the measured values.
- Over the period of the first fecal sample (about 0 - 0.1 d after intake), the predicted fecal excretion rate is more than *an order of magnitude lower* than the measured rate.
- After the measured "peak" in fecal excretion of uranium (during the first day), the *measured* excretion rate is about an order of magnitude *lower* than that *predicted*.

The above observations suggest that BOTH the measured urinary AND fecal excretion rates are strongly influenced by a relatively high "background" excretion of uranium. Since, in this case, continuous workplace air monitoring did NOT indicate the presence of chronic airborne contamination, in order to "fit" the observed excretion values, it is necessary to consider another *relatively constant* source of intake. The obvious candidate is *dietary intake*.

D.5.5. Correct for Dietary Uranium Intake

Figure D.77 shows the result of analysing jointly the measured urinary and fecal excretion rates, under the assumption that a single acute inhalation of Type 'S' uranium (Figure D.76) is superimposed on a long-term (uniform chronic) intake of uranium in the diet. The chronic intake is defined by:

- A uniform chronic ingestion of uranium with a gut uptake fraction, $f_1 = 0.02$, i.e., an "unknown" form of uranium - commencing 20 y prior to the inhalation intake - and continuing beyond the bioassay monitoring period.

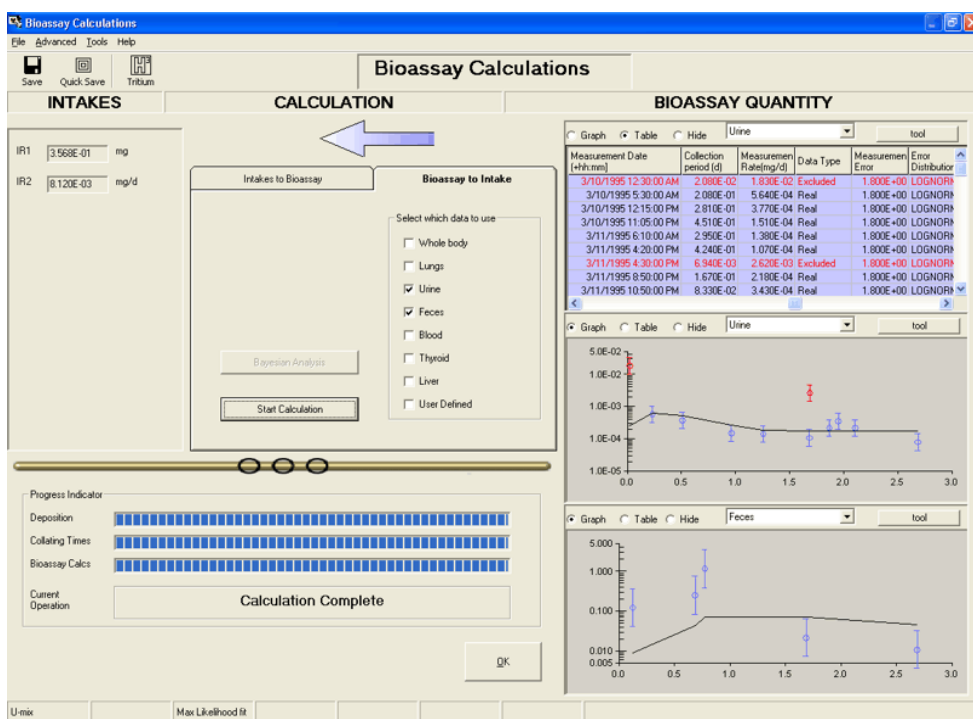


Figure D.77. Data "fit" for assumed combination of acute inhalation with **background chronic ingestion**.

Findings from plotted data fits

The resulting data fits (Figure D.77) show clearly that:

- The assumption of chronic "background" intake (by ingestion) significantly improves the "fit" to the urinary excretion data.
- The "peak" values of fecal excretion rate (within a day of the inhalation intake) are substantially "under-predicted" - and the fecal excretion rates measured over the following 2 days are substantially "over-predicted."

These observations indicate that the chronic mass intake rate must have been substantially higher than the value (of about 8 $\mu\text{g/d}$) fitted on the assumption of 'moderate' absorption (corresponding to the assumed f_1 value of 0.02). In fact, the data shows that the early fecal excretion rates were about an order of magnitude *higher* than the fitted rates - without significantly influencing urinary excretion. This can only happen if the chronically ingested material has a substantially lower value of f_1 than we assumed here, *i.e.*, the dietary uranium is *significantly less readily absorbed*. So, we can expect to improve the data "fit" by *finding* more appropriate parameter values, *i.e.*, by *optimizing the intake model*.

D.5.6. Optimize Intake Model Parameters

In reality, the "background" dietary intake would have been "natural" uranium, and not "LEU" - as assumed in the previous analysis. Therefore a different conversion factor to mass should have been applied to the "baseline" fecal excretion rates (measured and reported as "pCi/d"). The "background" uranium mass excretion rates should be higher by a factor of about 3.55 - in the ratio of the specific activities of LEU:U-Nat (approximately 2,422:683). Accordingly, before "optimizing" the data "fit", the "input" uranium mass excretion rates representing the "baseline" uranium excretion should be adjusted - as shown in Figure D.78.

Untitled - Notepad

3/10/1995 3:00:00 AM	1.250E-01	1.220E-01	Exc	3.000E+00	LOGNORM
3/10/1995 3:00:00 AM	1.250E-01	4.330E-01	Real	3.000E+00	LOGNORM
3/10/1995 4:30:00 PM	5.630E-01	2.500E-01	Real	3.000E+00	LOGNORM
3/10/1995 6:35:00 PM	8.680E-02	1.140E+00	Real	3.000E+00	LOGNORM
3/11/1995 4:30:00 PM	9.130E-01	2.170E-02	Exc	3.000E+00	LOGNORM
3/12/1995 4:30:00 PM	1.000E+00	1.090E-02	Exc	3.000E+00	LOGNORM
3/11/1995 4:30:00 PM	9.130E-01	7.700E-02	Real	3.000E+00	LOGNORM
3/12/1995 4:30:00 PM	1.000E+00	3.870E-02	Real	3.000E+00	LOGNORM

Figure D.78. Adjusting the 1st, 4th and 5th values of uranium mass excretion rates for the specific activity of natural uranium.

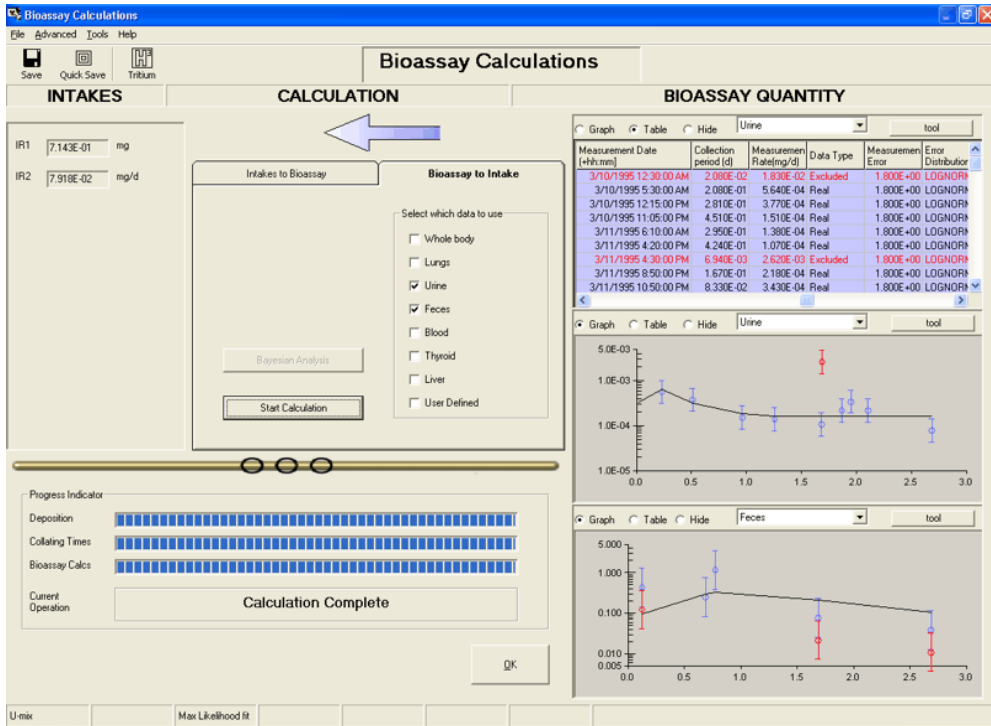


Figure D.79. Data "fit" obtained by "optimizing" intake and GI-tract model parameter values - with adjusted "baseline" fecal uranium mass excretion rates.

Figure D.79 shows the result of "optimizing" the data "fit" - by using the adjusted "baseline" fecal uranium mass excretion rates (Figure D.78) and manually varying the model parameters. The changes made to the model parameters were as follows:

1. Reducing the f_1 value for the acute inhalation (IR1) to **0.0002** (from the "default" value of 0.002).
2. Reducing the f_1 value for the "background" chronic dietary intake (IR2) to **0.002** (from the "default" value of 0.02).
3. Doubling the rate of transport through the SI to **12 d⁻¹** (from the "default" value of 6 d⁻¹).
4. Doubling the rate of transport through the ULI to **3.6 d⁻¹** (from the "default" value of 1.8 d⁻¹).
5. Doubling the rate of transport through the LLI to **2 d⁻¹** (from the "default" value of 1 d⁻¹).

Reasons for changes

- The first change reflects the high-fired (ceramic) nature of the airborne particles.
- The second change is necessary to improve the "fit" the adjusted "baseline" fecal excretion rate, i.e., after the "bolus" of inhaled LEU material has been excreted.

- The third, fourth and fifth changes (see Figure D.80) improve the "fit" to the observed "peak" in fecal excretion *within the first day*, and also predict a substantial reduction in fecal excretion over the following two days - down towards the adjusted "baseline" rates.

The screenshot shows the 'GI Tract Model' window with the 'User Defined' tab selected. The interface includes a flow diagram on the left and a list of rate constants on the right. The flow diagram shows a vertical stack of boxes: 'Blood' (pink), 'St' (yellow), 'SI' (yellow), 'ULI' (yellow), and 'LLI' (yellow). Arrows indicate the flow from 'St' to 'SI', 'SI' to 'ULI', 'ULI' to 'LLI', and a feedback arrow from 'SI' to 'Blood' labeled f_1 . The rate constants on the right are: Stomach (St) = 24, Small Intestine (SI) = 12, Upper large intestine (ULI) = 3.6, and Lower large intestine (LLI) = 2. A 'Clear' button is below these. At the bottom right, f_1 is set to 0.0002. At the bottom left, there are buttons for 'User Defined' (selected), 'LOAD ICRP DEFAULTS', 'OK', and 'Cancel'.

Figure D.80. "User Defined" values of rate constants in the GI Tract model.

Important Note: The interpretation of the data developed here in this example case is not intended to be "definitive." *It has NOT been reviewed by USDOE nor any other Regulatory Authority.* It is intended merely to illustrate the flexibility and power provided in [IMBA Expert™ OCAS/ORAU-Edition](#) - which enables YOU to "test" the effects of reasonable "hypotheses" about the conditions of intake and other "model" parameters. You are invited to investigate this example further - in order to draw your own conclusions!

D.5.7. Committed Doses from U-Mixture

Our "optimized" estimates (Figure D.79) of the components of uranium intake (by mass) in this example are:

- Acute inhalation of LEU (**0.714 mg**) at 0:00 AM on March 10th, 1995.
- Chronic dietary intake (natural uranium) of **79.2 $\mu\text{g d}^{-1}$** (assumed here to have started at 0:00 AM on March 10th, 1975).

As for all dose calculations, for this "**Uranium Mixture**" case, you calculate the resulting committed doses by *clicking* the "Dose Calculations" button in the **Main Screen** (Figure D.81) - to open the "Dose Calculations" screen. In this case, we are only interested in the "occupational" dose from the acute intake of LEU (**IR1**).

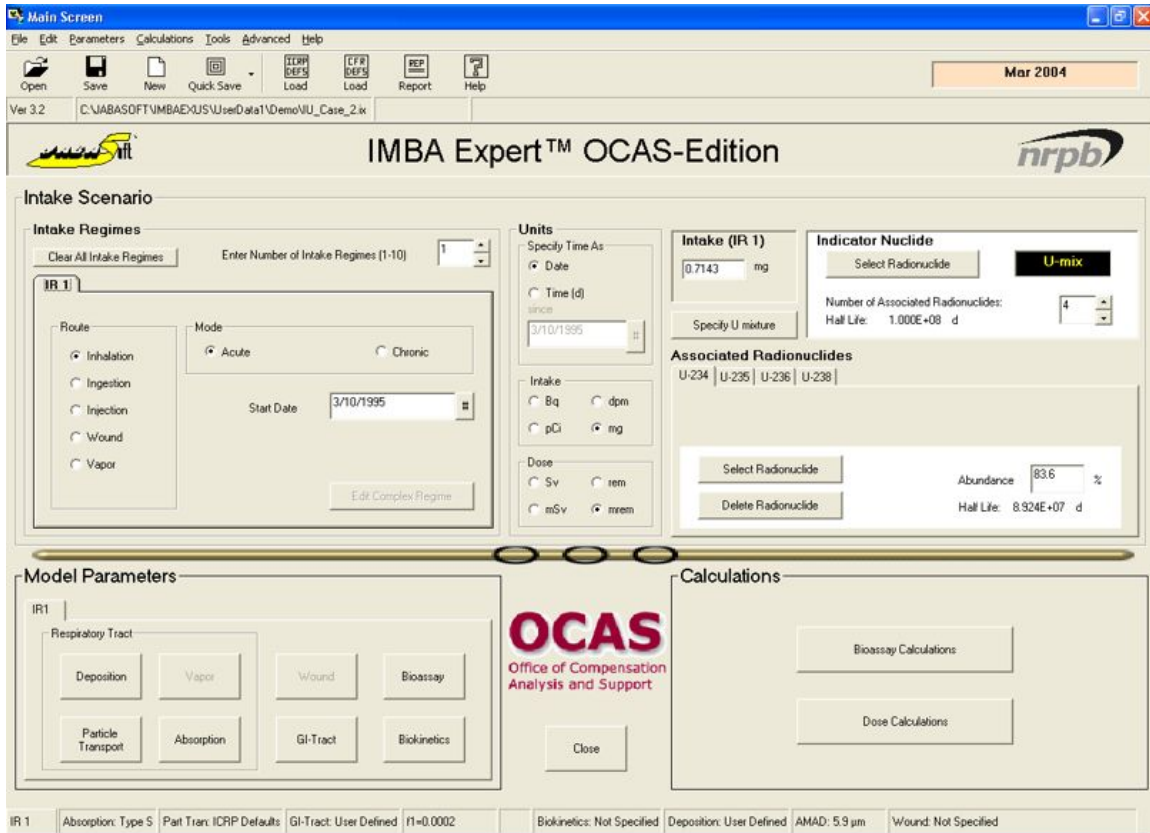


Figure D.81. "Dose Calculations" button for calculating committed doses for a **Uranium Mixture** (treated as **Associated Radionuclides**).

For this example, we have:

- Checked "**mrem**" as the dose unit (Figure D.81).
- Reduced the number of intake regimes to ONE (**IR1**) - also shown in Figure D.81.
- Selected the "**ICRP Default**" values of radiation weighting factor (w_R) - in the "**Dose Calculations**" screen.
- Selected the "**10CFR835 Default**" values of tissue weighting factor (w_T).
- Checked the "**Dose from Associated Radionuclides**" box .
- Checked the "**Dose Committed in Each Calendar Year**" box.
- Selected the "**Speed**" calculation option from the **Advanced | Advanced Dosimetry Options | Dose** menu (Figure D.82 - see also **Appendix A: Effect of Merging SEEs**).
- Clicked the "**Calculate**" button.

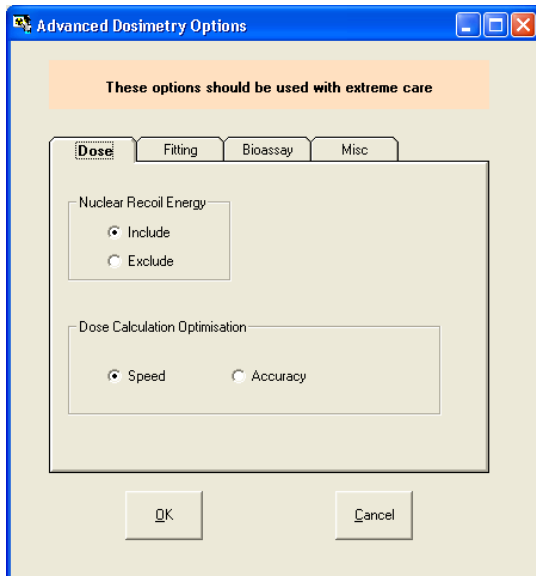


Figure D.82. Selecting the "Speed" option - to "merge" the initial short-lived progeny of ^{235}U and ^{238}U .

Note: In this case (and in all "practical" cases) you should use the "Speed" option to calculate doses from intakes of ^{235}U and ^{238}U . This option "merges" the disintegrations of the initial short-lived progeny of these uranium isotopes - and represents more closely the actual situation - where these short-lived progeny are taken into the body in radioactive equilibrium with the parent uranium isotope. The "Accuracy" option assumes that ONLY the parent uranium isotopes are taken into the body - which is the case ONLY for ICRP-published "dose coefficients" (see **Appendix C: Dose Quality Assurance** for discussion). Not only will the "Accuracy" option give the wrong answers, but the dose calculation will take a lot longer to complete - because of the wasted time spent calculating progeny in-growth!

The resulting calculated doses are shown in Figure D.83.

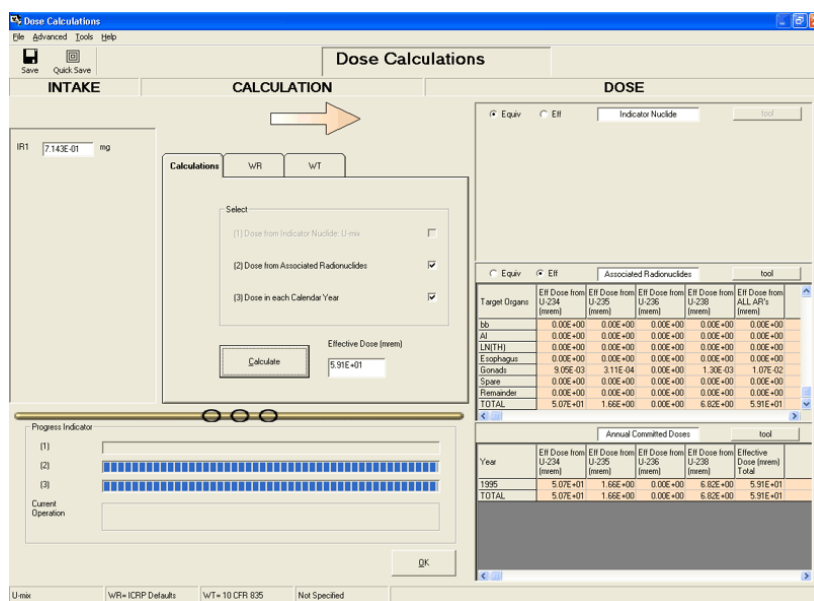


Figure D.83. Calculated total effective dose together with the year in which it was committed.

Figure D.83 shows that:

- The committed effective dose from the estimated acute intake of LEU ($IR1 = 0.714 \text{ mg}$) is **59.1 mrem**.

D.5.8. Published Data on Background U-in-Urine

In this case, the average of the measured (background) uranium mass excretion rates in urine was **0.19 $\mu\text{g/d}$** , with a standard deviation of **0.11 $\mu\text{g/d}$** - see the 6th and 8th through 11th values in the data tabulation (Figure D.74). The reported ranges of the "background" urinary excretion rate for dietary uranium are:

- **0.01 - 0.05 $\mu\text{g/d}$** (Karpas et al 1996).
- **0.005 - 0.5 $\mu\text{g/d}$** (Dang et al 1992).
- **0.035 - 0.085 $\mu\text{g/d}$** (CDC 2001) - U.S. Population.



Note: The above data were reported as volumetric concentration ($\mu\text{g/L}$). They have been converted here to the daily excretion rate, assuming the **New Reference Man** (ICRP 2002b) value of **1.6 L/d** urinary output.

In their **2004 Information Paper**¹, the Department of Defense (DoD) assumed a "typical" background excretion rate (for dietary uranium in urine) of **0.05 $\mu\text{g/d}$** . The value of **0.19 $\mu\text{g/d}$** , that we have associated in this example with background excretion of dietary uranium is therefore about four-fold higher than the DoD's estimate of the typical value for a member of the U.S. population, *i.e.*, it is double the upper bound value reported by CDC (2001). Therefore, the "background" urinary excretion of uranium in urine measured in this example case may well include a substantial component from past "occupational" uranium exposure.

D.5.9. Uranium Example Case Summary

In summary, it is instructive to compare the estimates of committed effective dose obtained at each stage of the analysis for this case.

Assuming single acute inhalation intake of Type 'S' LEU

- Joint analysis of the measured urinary and fecal uranium mass excretion rates (without correction for "background" excretion) gave an estimated LEU intake of **2.055 mg** - with a corresponding committed effective dose of **170 mrem**.

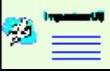
Assuming acute inhalation of Type 'S' LEU - together with chronic dietary intake (f_1 value of 0.02)

- Joint analysis of the measured urinary and fecal uranium mass excretion rates gave an estimated (acute) LEU intake of **0.357 mg** - with a corresponding committed effective dose of **29.6 mrem**.

¹ http://www.deploymentlink.osd.mil/du_library/lab_assessment/lab_assessment_s02.htm.

"Optimizing" the model parameters

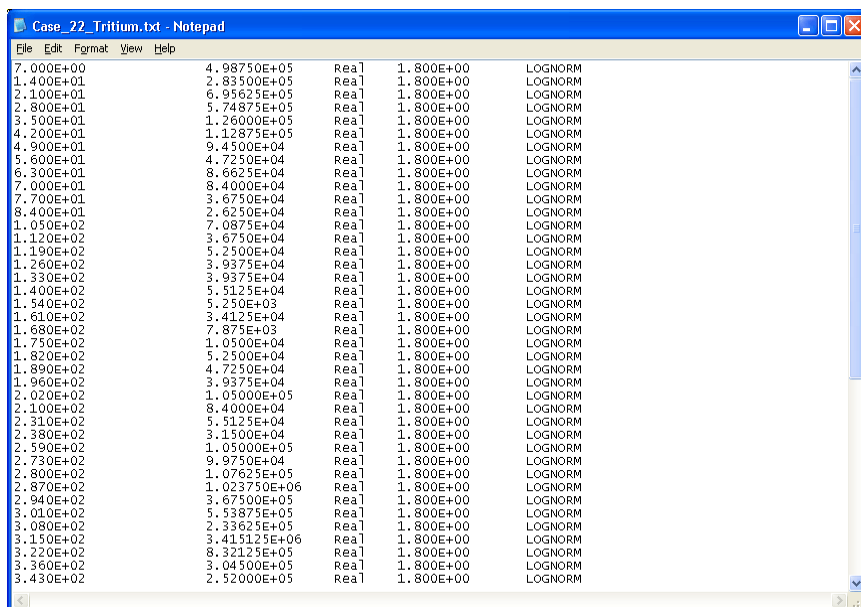
- Joint analysis of the measured urinary and (adjusted) fecal uranium mass excretion rates gave an estimated (acute) LEU intake of **0.714 mg** - with a corresponding committed effective dose of **59.1 mrem**.

	Note #1: Least squares analysis only of the measured urinary uranium mass excretion rates (including the two "outlying" data points) together with the reported normal (counting) errors - as is the common practice - gave an estimated LEU intake (assuming acute inhalation of Type 'S' uranium) of 0.575 mg (± 0.246 mg standard error). The corresponding estimate of committed effective dose is 47.6 mrem (± 20.4 mrem standard error). In this case, reasonable agreement with the value of 59.1 mrem derived by more exhaustive analysis is fortuitous.
	Note #2: The value of 0.575 mg acute LEU intake obtained using the <i>least squares</i> fitting method in IMBA Expert™ OCAS/ORAU-Edition is identical to the value given by the software package IMBA-URAN (for the same model assumptions). As expected, the identical value is also obtained using the <i>maximum likelihood</i> fitting method (in IMBA Expert™ OCAS/ORAU-Edition).

D.6. Routine Tritium Urinalysis

This case is an example of routine tritium urinalysis (for exposure to tritium vapor - HTO) carried out over a 553-d period on a weekly sampling schedule. The case is taken from the European **IDEAS project** (Case #22) – see Doerfel et al (2003) and also <http://hikwww2.fzk.de/hs/strahlenschutz/IDEAS/default.htm>.

The urinalysis data (ready for importing into **IMBA Expert™ OCAS/ORAU-Edition**) is provide in the ACSII text file "**Case_22_Tritium.txt**" - - which is included in the **[Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo** folder at installation. The first part of this file is shown in Figure D.84.



7.000E+00	4.98750E+05	Real	1.800E+00	LOGNORM
1.400E+01	2.83500E+05	Real	1.800E+00	LOGNORM
2.100E+01	6.95625E+05	Real	1.800E+00	LOGNORM
2.800E+01	5.74875E+05	Real	1.800E+00	LOGNORM
3.500E+01	1.26000E+05	Real	1.800E+00	LOGNORM
4.200E+01	1.12875E+05	Real	1.800E+00	LOGNORM
4.900E+01	9.4500E+04	Real	1.800E+00	LOGNORM
5.600E+01	4.7250E+04	Real	1.800E+00	LOGNORM
6.300E+01	8.6625E+04	Real	1.800E+00	LOGNORM
7.000E+01	8.4000E+04	Real	1.800E+00	LOGNORM
7.700E+01	3.6750E+04	Real	1.800E+00	LOGNORM
8.400E+01	2.6250E+04	Real	1.800E+00	LOGNORM
1.050E+02	7.0875E+04	Real	1.800E+00	LOGNORM
1.120E+02	3.6750E+04	Real	1.800E+00	LOGNORM
1.190E+02	5.2500E+04	Real	1.800E+00	LOGNORM
1.260E+02	3.9375E+04	Real	1.800E+00	LOGNORM
1.330E+02	3.9375E+04	Real	1.800E+00	LOGNORM
1.400E+02	5.5125E+04	Real	1.800E+00	LOGNORM
1.540E+02	5.250E+03	Real	1.800E+00	LOGNORM
1.610E+02	3.4125E+04	Real	1.800E+00	LOGNORM
1.680E+02	7.875E+03	Real	1.800E+00	LOGNORM
1.750E+02	1.0500E+04	Real	1.800E+00	LOGNORM
1.820E+02	5.2500E+04	Real	1.800E+00	LOGNORM
1.890E+02	4.7250E+04	Real	1.800E+00	LOGNORM
1.960E+02	3.9375E+04	Real	1.800E+00	LOGNORM
2.020E+02	1.05000E+05	Real	1.800E+00	LOGNORM
2.100E+02	8.4000E+04	Real	1.800E+00	LOGNORM
2.310E+02	5.5125E+04	Real	1.800E+00	LOGNORM
2.380E+02	3.1500E+04	Real	1.800E+00	LOGNORM
2.590E+02	1.05000E+05	Real	1.800E+00	LOGNORM
2.730E+02	9.9750E+04	Real	1.800E+00	LOGNORM
2.800E+02	1.07625E+05	Real	1.800E+00	LOGNORM
2.870E+02	1.02375E+06	Real	1.800E+00	LOGNORM
2.940E+02	3.67500E+05	Real	1.800E+00	LOGNORM
3.010E+02	5.53875E+05	Real	1.800E+00	LOGNORM
3.080E+02	2.33625E+05	Real	1.800E+00	LOGNORM
3.150E+02	3.415125E+06	Real	1.800E+00	LOGNORM
3.220E+02	8.32125E+05	Real	1.800E+00	LOGNORM
3.360E+02	3.04500E+05	Real	1.800E+00	LOGNORM
3.430E+02	2.52000E+05	Real	1.800E+00	LOGNORM

Figure D.84. ASCII text file of input data for tritium urinalysis case.

In this example, we will:

- Use the whole dataset to determine individual intake events - and the resulting effective doses. This is the way that [IMBA Expert™ OCAS/ORAU-Edition](#) is used for most radionuclides.
- Use the special routine tritium urinalysis 'tool' to calculate intakes and resulting doses automatically - from sub-sets of urinalysis data.
- Compare doses estimated by these two different methods.

D.6.1. Determine Individual Tritium Intakes and Resulting Doses

This is done in [IMBA Expert™ OCAS/ORAU-Edition](#) by:

- Setting up the required "HTO" models.
- Identifying and "fitting" discrete intake events.
- Calculating doses from HTO intakes.

You can also use [IMBA Expert™ OCAS/ORAU-Edition](#) to:

- Calculate doses committed over several monitoring periods.

This feature is used in this example to provide "benchmark" values of committed dose - in order to "test" the values of dose calculated *directly* (from the HTO urinalysis data) using the routine tritium urinalysis "tool".

D.6.2. Setting Up the HTO Models

Figure D.85 shows the **Main Screen** of [IMBA Expert™ OCAS/ORAU-Edition](#) as set up to analyze the input data. The setup steps are:

- *Select "H(i)-3" as the **Indicator Nuclide** - i.e., inorganic tritium (HTO).*
- *Specify "**Time (d) since**" (the Start Date) as **9/25/1986**.*
- *Select "**10**" **Intake Regimes**.*
- *Define **All Intake Regimes** as "**Injection**" - ICRP treats inhalation of HTO as *injection* - see Appendix A: Assumed Metabolism of Tritiated Water.*
- *Click the "**Load ICRP DEFS**" button - this loads the "**Std H(i)**" bioassay model (Figure D.86) defining retention of HTO in the "bioassay quantity" (**Whole Body**) - and also the "**ICRP Default H(i)**" biokinetic model (Figure D.87) defining HTO retention in the blood, bladder and whole body (WB) - for dosimetry.*

Main Screen

File Edit Parameters Calculations Tools Advanced Help

Open Save New Quick Save Load Load Load Report Help

Ver 3.2 C:\IMBASOFT\IMBAEXUS\UserData1\Demo\Case22 - HTO - MP.k

Mar 2004

IMBA Expert™ OCAS-Edition

nrpb

Intake Scenario

Intake Regimes

Clear All Intake Regimes Enter Number of Intake Regimes (1-10) 10

IR 1 IR 2 IR 3 IR 4 IR 5 IR 6 IR 7 IR 8 IR 9 IR 10

Route: ☐ Inhalation ☐ Ingestion ☒ Injection ☐ Wound ☐ Vapor

Mode: ☐ Acute ☒ Chronic

Start Time (d) 502

End Time (d) 530

Units

Specify Time As: ☐ Date ☒ Time (d) since 9/25/1986

Intake: ☒ Bq ☐ dpm ☐ pCi ☐ mg

Dose: ☒ Sv ☐ rem ☐ mSv ☐ mrem

Intake (IR 10)

13648 Bq/d

Indicator Nuclide

Select Radionuclide: **H(0)-3**

Number of Associated Radionuclides: 0

Half Life: 4.508E+03 d

Associated Radionuclides

None Selected

Model Parameters

These Model Parameters Apply to All IRs

Respiratory Tract: Deposition Vapor Wound Bioassay

Particle Transport Absorption GI Tract Biokinetics

OCAS
Office of Compensation
Analysis and Support

Close

Calculations

Bioassay Calculations

Dose Calculations

All IRs Absorption: Type F Part Trans: ICRP Defaults GI Tract: ICRP Defaults f1=1 Biokinetics: ICRP H(i) Model Deposition: ICRP Defaults N/A Wound: Not Specified

Figure D.85. Main Screen setup for analysis of 10 discrete intakes of inorganic tritium vapor (HTO).

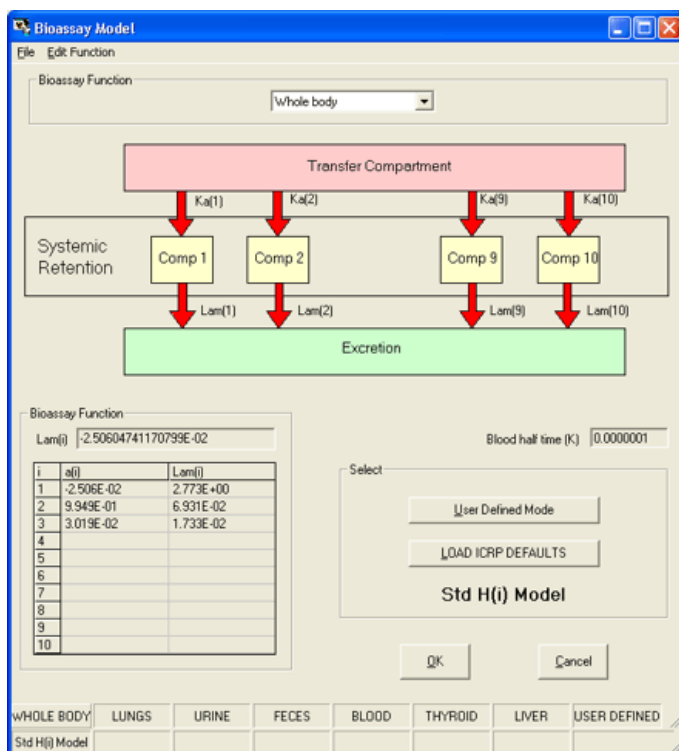


Figure D.86. ICRP's "Standard H(i) Model" for HTO bioassay (Whole Body retention).

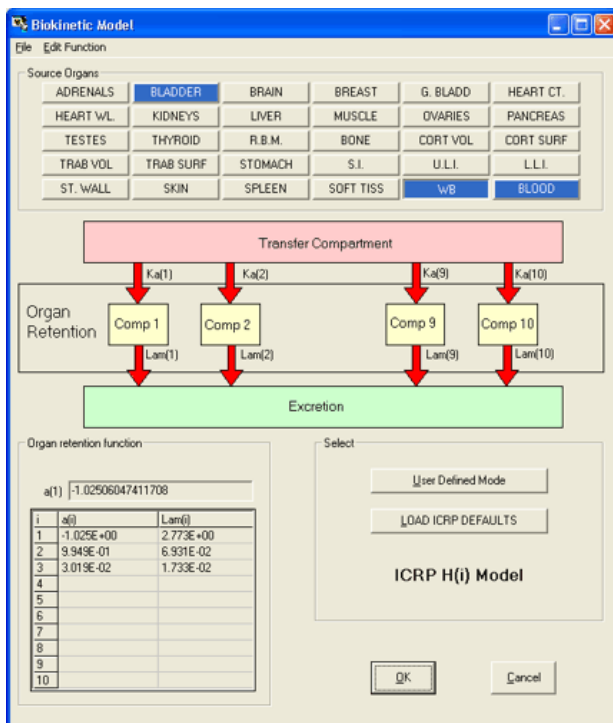


Figure D.87. Default "ICRP H(i) Model" for HTO biokinetics.

D.6.3. Fitting Discrete HTO Intake Events

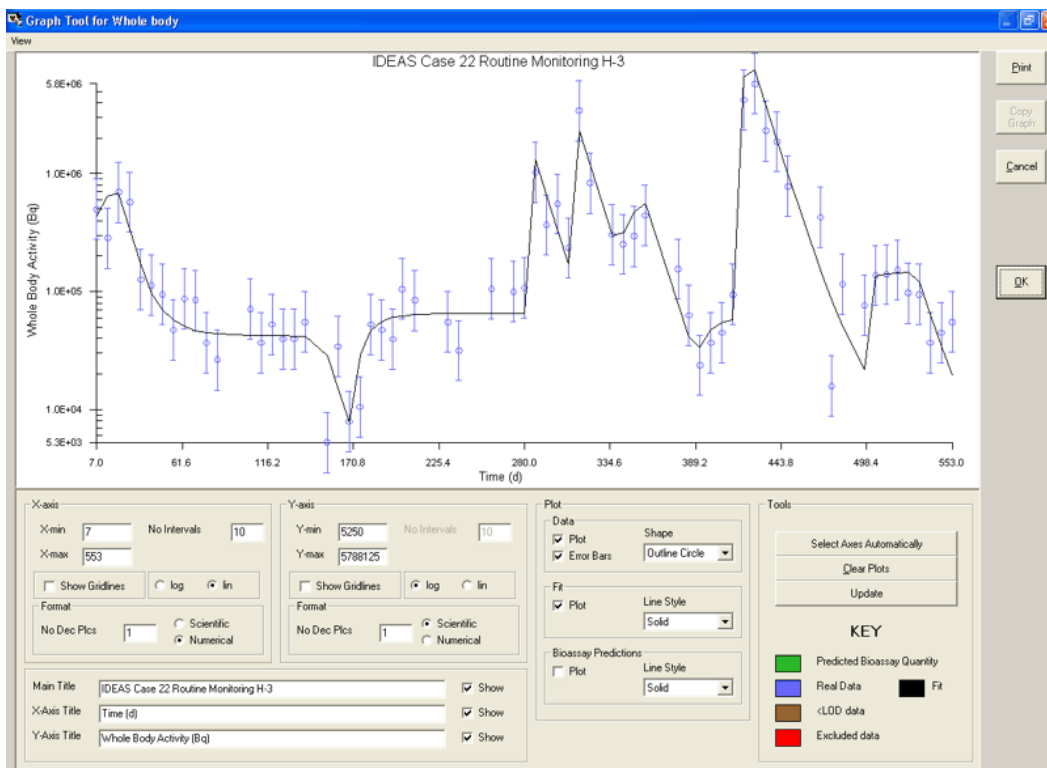


Figure D.88. Routine tritium urinalysis data together with 'fit' obtained by assuming 10 separate intake events.

Figure D.88 shows the result of an analysis of the variation of whole body retention of HTO at the time of each weekly urine sample carried out for the IDEAS Project (personal communication, Dr. M. Puncher, NRPB). **Note that:** the whole body retention is calculated on the assumption that the concentration of HTO in all body tissues is in equilibrium with, *i.e.*, equal to, that in urine. [IMBA Expert™ OCAS/ORAU-Edition](#) allows up to **10** discrete intakes to be defined. In this case, it was necessary to use **all 10** in order to "fit" the major temporal features of the bioassay data.

The "fitting" process is not as complicated as it might appear to be. Since HTO is eliminated rather rapidly from the body (97% with an assumed 10-d half-time, with 3% retained with a 40-d half-time - see **Appendix A: Assumed Metabolism of Tritiated Water**), there is relatively little "carry over" of HTO through to monitoring periods several weeks into the future. The "fitting" process is therefore carried out *iteratively* - starting with the earliest monitoring results. Once a reasonable "fit" is obtained to the first "temporal pattern" of HTO retention - by postulating either an "acute" intake at an assumed time - or "chronic" intake over an assumed time-range (and leaving all "future" intakes *undefined*) - you can repeat this process for the second "temporal pattern". In order to "fit" both patterns, you will probably have to refine your assumptions (somewhat) about the timing of the first intake event.



Note: It is only necessary for you to "guess" the temporal parameters of each postulated intake. [IMBA Expert™ OCAS/ORAU-Edition](#) automatically calculates the resulting value(s) of the intake amount(s) (in the bioassay data to intakes mode of the **Bioassay Calculations** screen) - to give the "most likely" fit to the data. This is a surprisingly quick process - once you get the hang of it!

Figure D.89 shows this "solution" of the progressive "fitting" task.

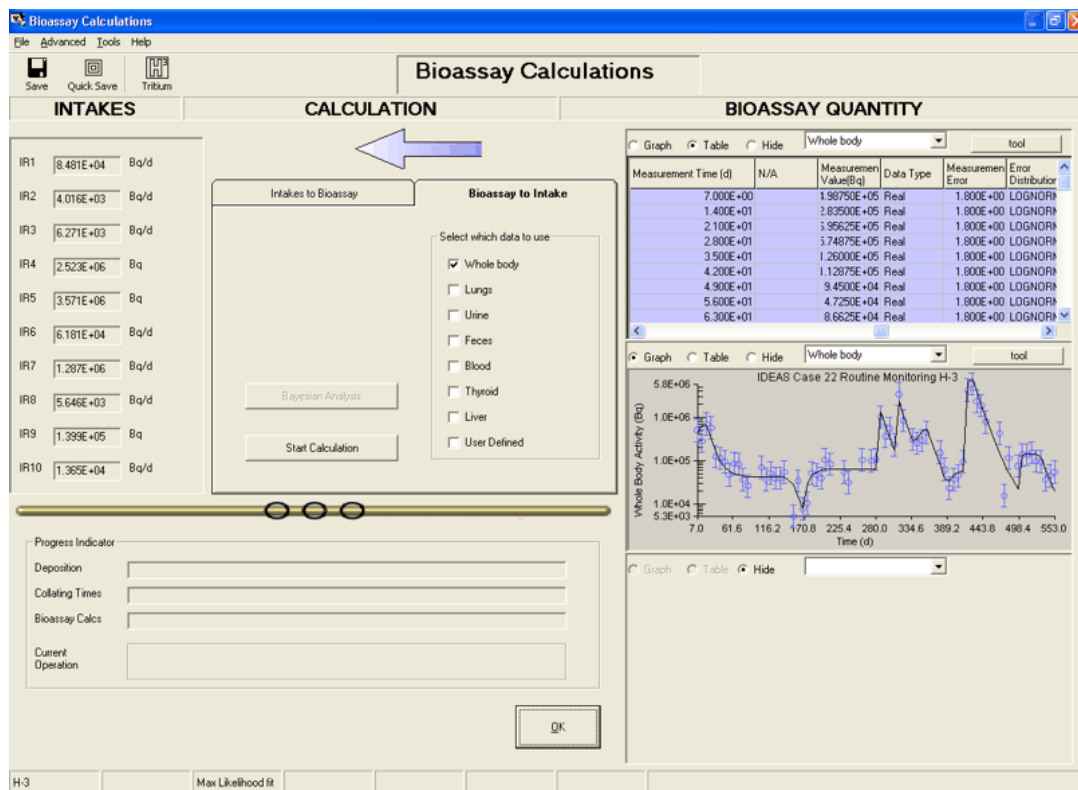


Figure D.89. Calculated intakes (*IR1 through IR10*) for tritium urinalysis case.

The "best estimates" of the **10 discrete intakes** that gave rise to the observed HTO retention pattern are:

Table D.7. Discrete intake calculated from the tritium urinalysis data.

Intake regime	Assumed timing	Intake amount/rate (Bq/Bq d ⁻¹)
IR1 - chronic	0 - 20 d	84,810 Bq/d
IR2 - chronic	40 - 150 d	4,016 Bq/d
IR3 - chronic	170 - 280 d	6,271 Bq/d
IR4 - acute	280 d	2,530,000 Bq
IR5 - acute	310 d	3,571,000 Bq
IR6 - chronic	340 - 357 d	61,810 Bq/d
IR7 - chronic	413 - 425 d	1,287,000 Bq/d
IR8 - chronic	390 - 440 d	5,646 Bq/d
IR9 - acute	500 d	139,900 Bq
IR10 - chronic	502 - 530 d	13,650 Bq/d



Tip: Try this fitting process *yourself* - from "scratch" - using the raw input data (by importing the ASCII text data file [Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo\Case_22_Tritium.txt into the Table Tool). The "solution" above is saved in the parameter file "Case22 - HTO - MP.ix" (in the same folder).

D.6.4. Calculating Doses from HTO Intakes

Dose Tool : Effective Doses (H-3)											
Target Organs	Cont. to Eff Dose (Sv) IR(1)	Cont. to Eff Dose (Sv) IR(2)	Cont. to Eff Dose (Sv) IR(3)	Cont. to Eff Dose (Sv) IR(4)	Cont. to Eff Dose (Sv) IR(5)	Cont. to Eff Dose (Sv) IR(6)	Cont. to Eff Dose (Sv) IR(7)	Cont. to Eff Dose (Sv) IR(8)	Cont. to Eff Dose (Sv) IR(9)	Cont. to Eff Dose (Sv) IR(10)	Effective Dose (Sv) Total
Adrenals	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Urinary Bladder	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	1.28E-07	3.49E-07	2.40E-05
Brain	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Breast	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	1.28E-07	3.49E-07	2.40E-05
Gall Bladder	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Heart Wall	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Kidneys	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Liver	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	1.28E-07	3.49E-07	2.40E-05
Muscle	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Ovaries	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Pancreas	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Testes	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Thyroid	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	1.28E-07	3.49E-07	2.40E-05
R.B.M.	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	3.07E-07	8.38E-07	5.75E-05
Bone Surface	3.10E-07	8.07E-08	1.26E-07	4.61E-07	6.52E-07	1.92E-07	2.82E-06	5.16E-08	2.58E-08	6.98E-08	4.79E-06
Stomach	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	3.07E-07	8.38E-07	5.75E-05
S.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
U.L.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
L.L.I.	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Skin	3.10E-07	8.07E-08	1.26E-07	4.61E-07	6.52E-07	1.92E-07	2.82E-06	5.16E-08	2.58E-08	6.98E-08	4.79E-06
Spleen	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Thymus	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Uterus	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
ET	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Lung	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	3.07E-07	8.38E-07	5.75E-05
Colon	3.72E-06	9.69E-07	1.51E-06	5.53E-06	7.83E-06	2.30E-06	3.39E-05	6.19E-07	3.07E-07	8.38E-07	5.75E-05
ET1	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
ET2	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
LN(ET)	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
BBsec	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
BBbas	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
bb	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
AI	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
LN(TH)	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Esophagus	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	1.28E-07	3.49E-07	2.40E-05
Gonads	6.20E-06	1.61E-06	2.52E-06	9.22E-06	1.30E-05	3.84E-06	5.64E-05	1.03E-06	5.11E-07	1.40E-06	9.58E-05
Spare	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Remainder	1.55E-06	4.04E-07	6.30E-07	2.30E-06	3.26E-06	9.60E-07	1.41E-05	2.58E-07	1.28E-07	3.49E-07	2.40E-05
TOTAL	3.10E-05	8.07E-06	1.26E-05	4.61E-05	6.52E-05	1.92E-05	2.82E-04	5.16E-06	2.58E-06	6.98E-06	4.79E-04

Figure D.90. Contributions to total effective dose from each HTO intake.

The contributions to the overall committed effective dose made by each of the 10 intakes (Figure D.90) is calculated simply in the **Dose Calculations** screen, in this example (Figure D.91) by:

- Selecting the "ICRP Default" radiation weighting factors (w_R).
- Selecting the "ICRP68" tissue weighting factors (w_T).

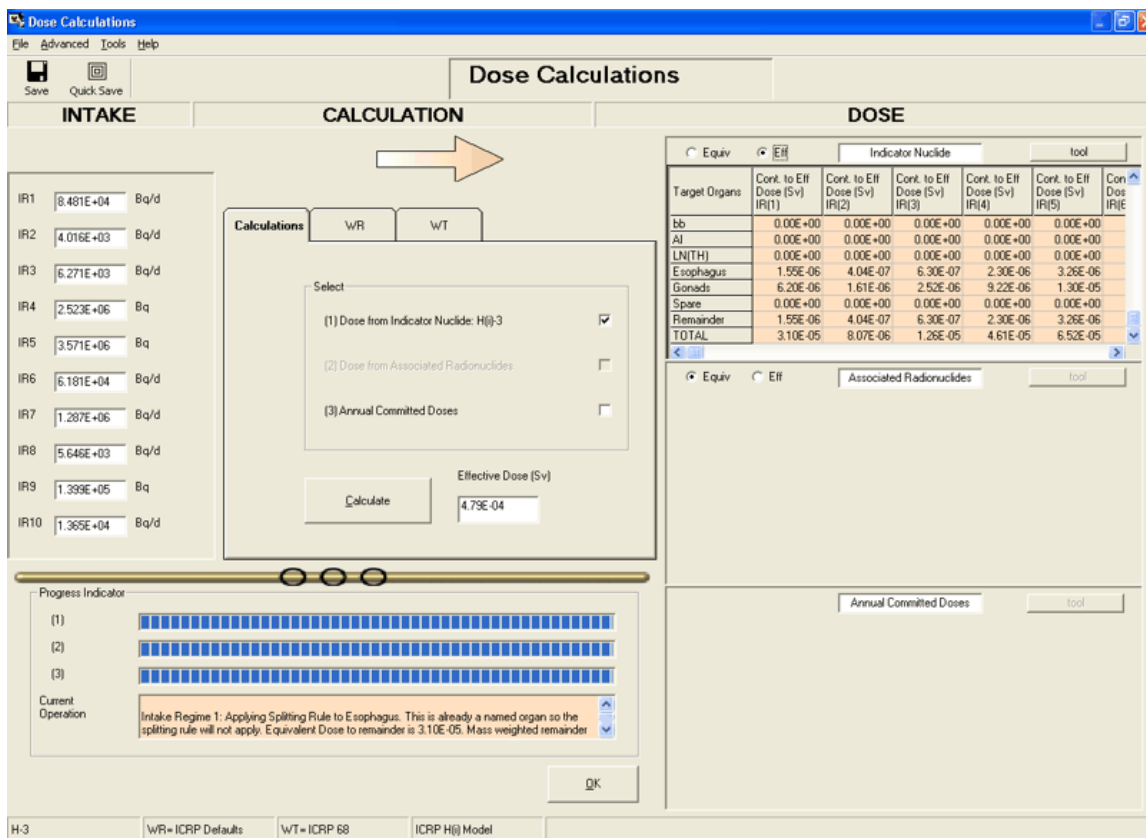


Figure D.91. Calculating and displaying both the contributions to effective dose from each HTO intake and the effective doses committed each year.



Note: In this example, the TOTAL (committed) effective dose is 4.79×10^{-4} Sv (479 μ Sv).

D.6.5. Dose Committed During HTO Monitoring Periods

The next section (Using the Routine Tritium Urinalysis 'Tool'), describes how to calculate committed doses *directly* from the tritium urinalysis data - without having first to determine (by manual fitting) the amounts of each discrete tritium intake. The urinalysis 'tool' analyzes up to 10 *sequential urinalysis results* - and calculates automatically the *total effective dose* committed over this *whole monitoring period*.

In this example, we can use the special feature provided in **IMBA Expert™ OCAS/ORAU-Edition** to calculate the **Annual Committed Doses** resulting from a series of intakes - to generate "benchmark" values of dose for comparison with the results obtained using the *Urinalysis "Tool"*. The 'Tool' analyzes a sequence of up to 10 *routine monitoring results*. In this example, the first

10 monitoring results covered the period from day "0" to day "70" (Figure D.84). In this example, we can calculate the total dose committed over just this initial 70-day period, by simply:

- Changing the "Start Date" (in the **Main Screen**) to [December 31st, 1986 - 70 d] = **October 22nd, 1986**.
- Re-calculating the "Annual Committed Doses".

Figure D.92 shows the resulting values of committed effective dose for the years 1986, 1987 and 1988. The value displayed for 1986 (**33.3 μ Sv**) corresponds to the effective dose committed during the first 70-d monitoring period.

Annual Committed Doses					
tool					
Year	Eff Dose from H(i)-3 (IN) (Sv)	Effective Dose (Sv) Total			
1986	3.33E-05	3.33E-05			
1987	4.36E-04	4.36E-04			
1988	9.95E-06	9.95E-06			
TOTAL	4.79E-04	4.79E-04			

Figure D.92. Annual committed doses in 1986, 1987 and 1988.



Tip: The effective dose committed during the first 70-d period of monitoring can also be calculated easily from the tabulated values of effective dose resulting from each discrete intake (Figure D.90) together with the tabulated duration of each intake (Table D.7). The required value is the *sum* of 31.0 μ Sv (from **IR1**) and $30/110 \times 8.1$ μ Sv (from **IR2**) = **33.2 μ Sv** (rounded). You can extract the dose committed during any other monitoring period in the same way.

D.6.6. Using the Tritium Monitoring 'Tool'

The **Tritium Routine Monitoring Tool** works independently of the standard "**Bioassay Data to Intake**" calculation mode (for determining the occurrence and amounts of *discrete tritium intakes*) that was described in the previous section. Here we will describe how you set up and use the *Tritium Routine Monitoring Tool* from "scratch" to calculate intakes and committed doses *automatically* from the **bioassay data**, in this case the *whole body retention of HTO* at a series of time-points that is derived from the urinalysis samples.

D.6.7. Setting Up the Tritium 'Tool'

After clicking the "New" button - or opening **IMBA Expert™ OCAS/ORAU-Edition** from its desktop icon - you first:

- Select "**H(i)-3**" - "inorganic tritium (HTO)" - as the **Indicator Nuclide**.

- Click the "ICRP DEFS Load" button.
- Click the "Bioassay Calculations" button.
- Select "Whole Body" as the bioassay data to use.
- Click the "H³ Tritium" button - top-left-corner of the **Bioassay Calculations** screen.

This will open the "Tritium Routine Monitoring Tool" window (Figure D.93).

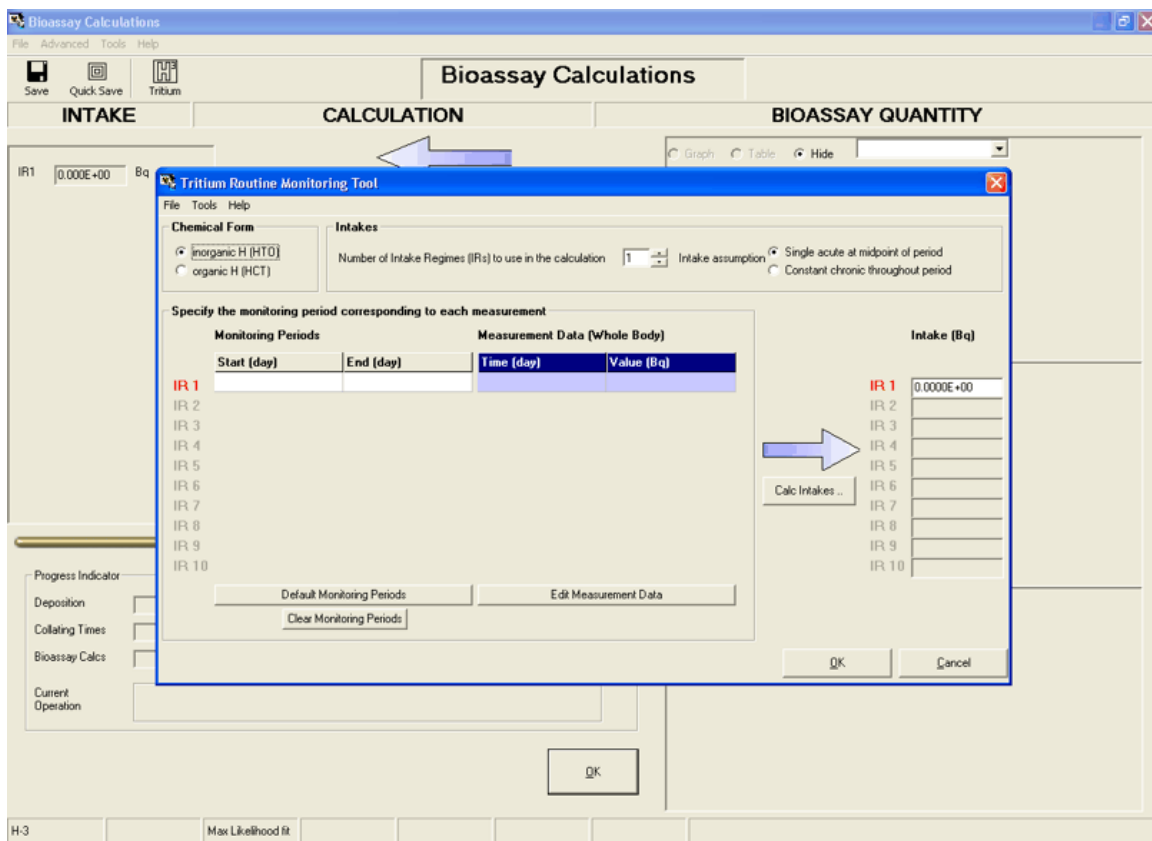


Figure D.93. Opening the Tritium Routine Monitoring Tool.

Note #1: This example considers only intakes of "inorganic H (HTO)" - for which the bioassay quantity is automatically set as "Measurement Data (Whole Body)". However, you also have the option to select "organic H (HCT)" from the *Tritium Routine Monitoring Tool*. In that case, the bioassay quantity will automatically be set as "Measurement Data (Urine)" - in the *Tritium Routine Monitoring Tool*, and "Urine Data" in the *Table Tool*.

Note #2: The *Tritium Routine Monitoring Tool* works independently of the **Indicator Nuclide** (which is selected in the **Main Screen**). None of the options selected in the "Tritium Tool" affect settings in the **Main Screen**.

You can use the **Tritium Routine Monitoring Tool** in two different ways:

1. To work on bioassay data already "loaded" in the **Table Tool**.
2. To work on bioassay data **imported** directly from an **external ASCII text file**.

The **Tritium Routine Monitoring Tool** is designed to simplify both ways of working, as follows:

- Using "pre-loaded" bioassay data - from the **Table Tool**.
- Using the "Import Wizard".

D.6.8. Loading Tritium Data Already in the Table Tool

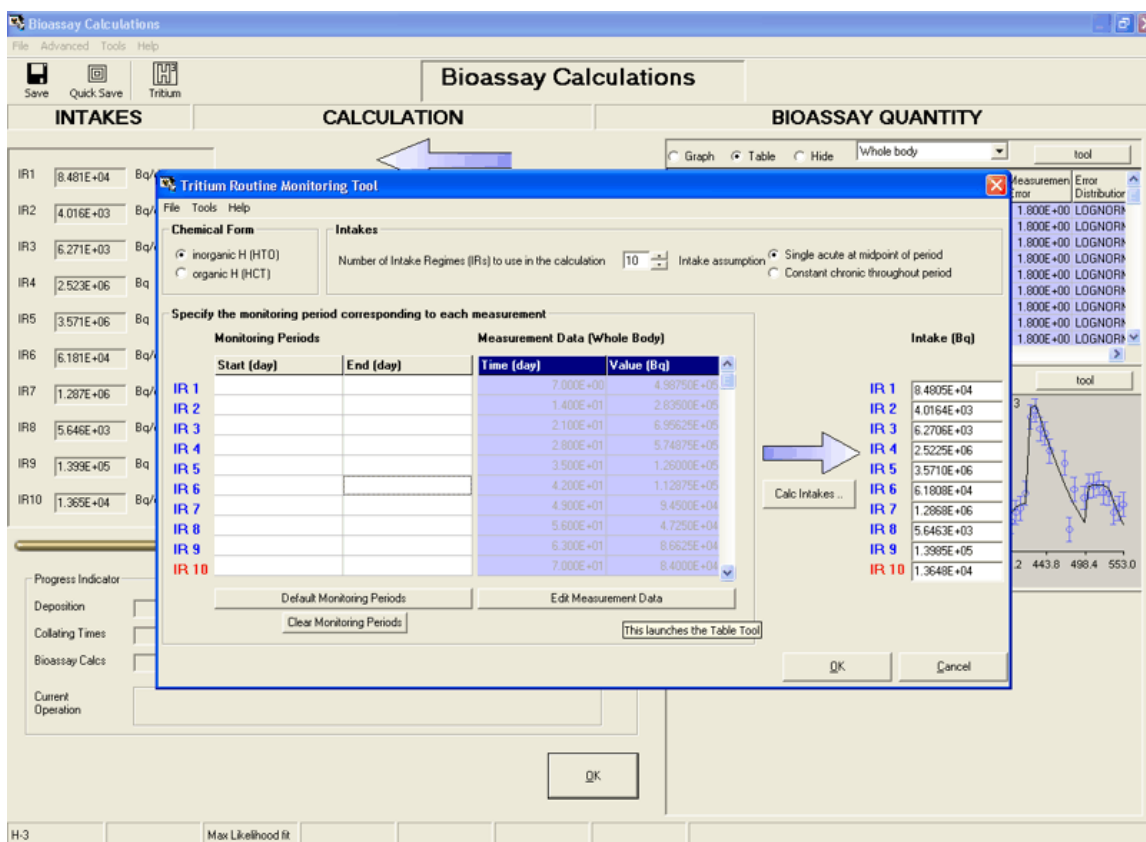


Figure D.94. Opening the **Tritium Routine Monitoring Tool** with "Whole Body" data already in the **Table Tool** - from "Case22 - HTO - MP.ix".

If you open the *Tritium Routine Monitoring Tool* when the **Table Tool** already contains bioassay data, in this case "Whole Body" data, the first 10 rows of "Time (day)" and "Value (Bq)" data will be displayed automatically in the tritium tool (Figure D.94) - under the heading "**Measurement Data (whole Body)**". The tritium tool will also display the last-calculated values of intake amounts (**IR1** through **IR10**) - under the heading "**Intake (Bq)**".

The *Tritium Routine Monitoring Tool* analyzes the bioassay data a *maximum* of 10 rows (i.e., 10 data points) at a time. Therefore, you need to *select* up to 10 rows of data from the **Table Tool** - *exclude* all other rows. Figure D.95 shows how you do this for rows 11 and below - by highlighting the corresponding "**Real**" entries in the "**Data Type**" column, *right-clicking* anywhere in the highlighted column, and *clicking* "**Excluded**".

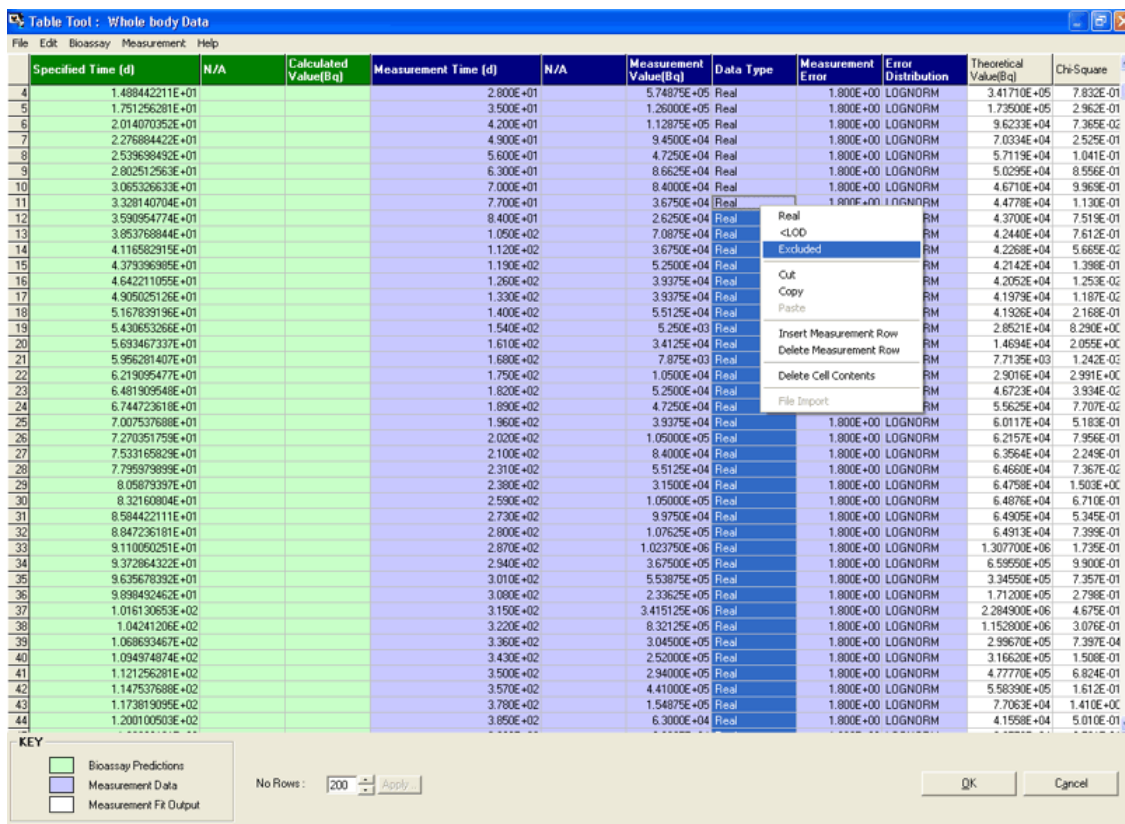


Figure D.95. Excluding all data in rows 11 and below in the Table Tool.

This will change the color of all data entries in row 11 and below to **red**, and also change the color of the corresponding data points plotted in the Bioassay Quantity graph (Figure D.96).

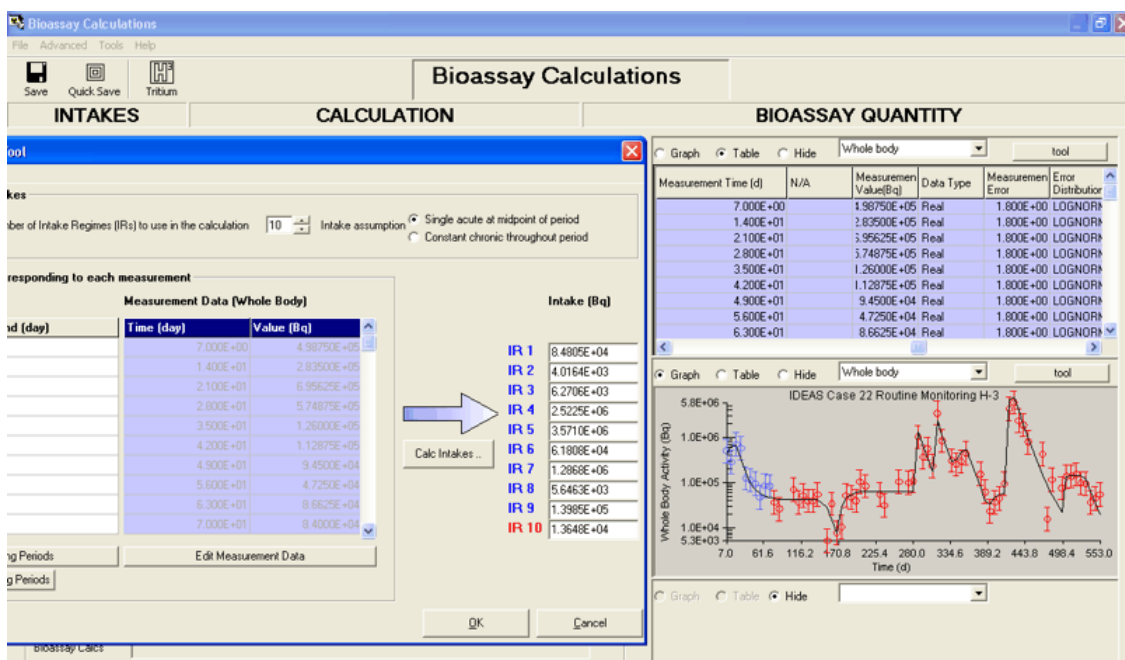
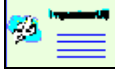


Figure D.96. Excluding the 11th and all further data points from analysis by the *tritium* tool.

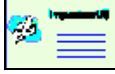
The next step is to "**Specify the monitoring period corresponding to each measurement**". If the sampling intervals are *contiguous*, the associated monitoring periods can be specified automatically - by simply *clicking* the "**Default Monitoring Periods**" button (as in Figure D.97).

Figure D.97. Specifying the monitoring periods automatically.

If the monitoring periods are not in fact all contiguous, you can edit any "**Start (day)**" value directly in the *Tritium Routine Monitoring Tool* table. Also, *clicking* the "**Edit Measurement Data**" button (Figure D.97) will return you to the **Table Tool** - so that you can *edit* any of the "input" bioassay data values. The functioning of the *Tritium Routine Monitoring Tool* is fully integrated with that of the **Table Tool**.



Warning: By default, the *Tritium Routine Monitoring Tool* assumes a "**Start (day)**" value of "**0**" - since the actual value is not included in the imported data. If "**0**" is incorrect, you will have to *enter* the appropriate value yourself. This is generally the "**End (day)**" of previous (most recent) set of monitoring data.



Note: You can *select ANY* sub-set of contiguous data rows (up to a maximum of 10 rows) from the **Table Tool** - for automatic *importation* into the *Tritium Routine Monitoring Tool*.

D.6.9. Loading Tritium Data with the 'Import Wizard'

Clicking the "**Edit Measurement Data**" button in the *Tritium Routine Monitoring Tool* opens the **Table Tool**. You can then *import* the required bioassay data (Figure D.98). In the **Table Tool**, *right-click* on the empty cell under the "**Measurement Time (d)**" heading (Figure D.98). From the drop-down menu, select "**File Import**" (as in Figure D.98). This will open the "ASCII file import wizard" (Figure D.99).

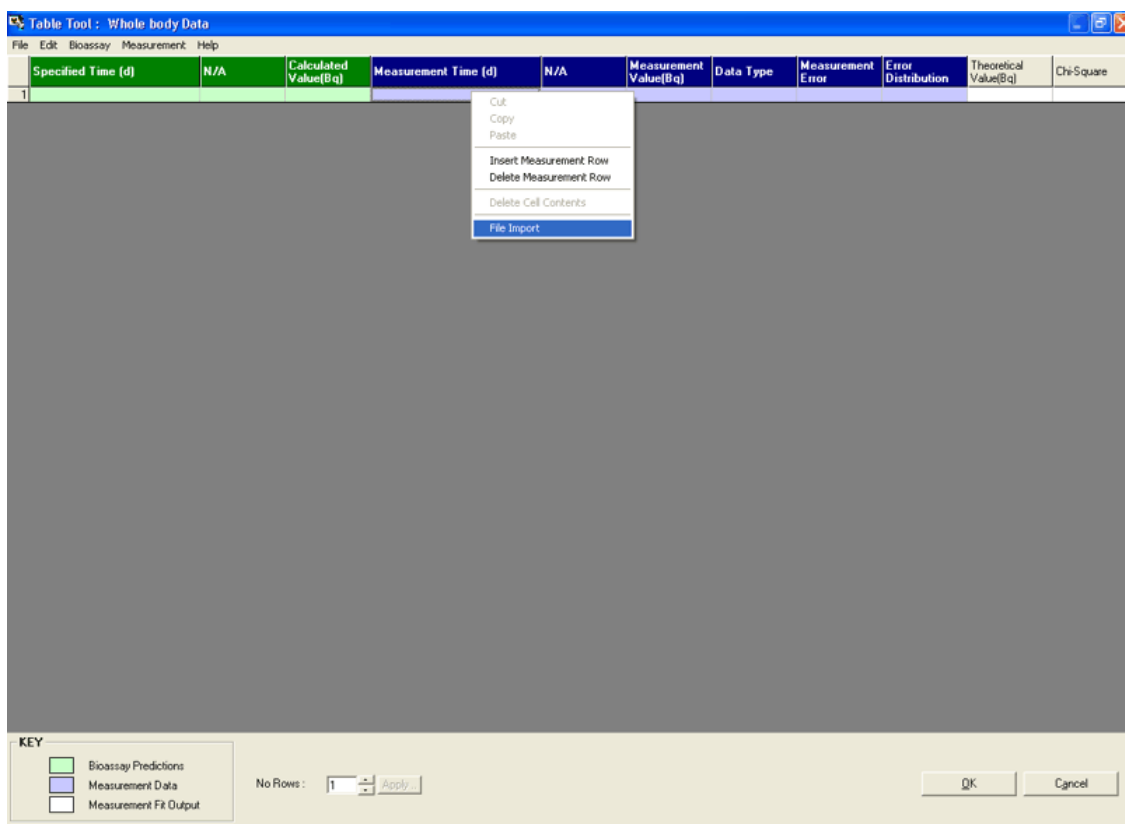


Figure D.98. Blank **Table Tool** ready to import a file of **whole body** bioassay data.

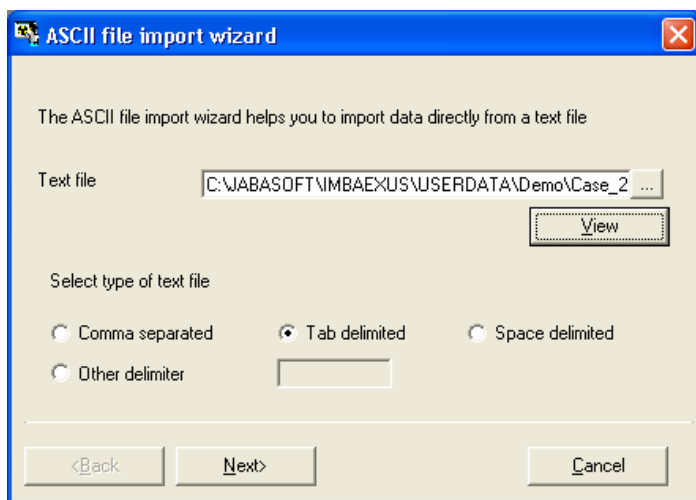


Figure D.99. The ASCII file **import wizard**.

In the ASCII file import wizard, *browse* to the folder **[Install Drv]:\JABASOFT\IMBAEXUS\USERDATA\Demo** and *select* the file "**Case_22_Tritium.txt**" data file, and *click* **V**iew (Figure D.99). This will open the file in NotePad® (Figure D.100).

Specified Time (d)	Measurement Value (Bq)	Data Type	Measurement Error	Error Distribution
7.000E+00	4.98750E+05	Real	1.800E+00	LOGNORM
1.400E+01	2.83500E+05	Real	1.800E+00	LOGNORM
2.100E+01	6.95625E+05	Real	1.800E+00	LOGNORM
2.800E+01	5.74875E+05	Real	1.800E+00	LOGNORM
3.500E+01	1.26000E+05	Real	1.800E+00	LOGNORM
4.200E+01	1.12875E+05	Real	1.800E+00	LOGNORM
4.900E+01	9.4500E+04	Real	1.800E+00	LOGNORM
5.600E+01	4.7250E+04	Real	1.800E+00	LOGNORM
6.300E+01	8.6625E+04	Real	1.800E+00	LOGNORM
7.000E+01	8.4000E+04	Real	1.800E+00	LOGNORM

D.100. First part of the "Case_22_Tritium.txt" data file - viewed in NotePad®.

This file is "tab delimited" - and so you need to *click* the "Tab delimited" button (Figure D.99) before *clicking* **Next**. The whole file will then be imported (into rows and columns) in the ASCII file import wizard (Figure D.101).

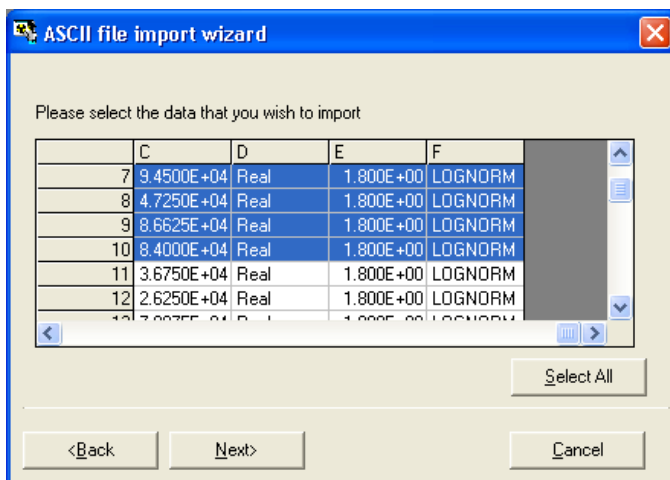


Figure D.101. Selecting the first 10 rows of data.

The **Tritium Routine Monitoring Tool** analyzes the bioassay data a *maximum* of 10 rows (i.e., 10 data points) at a time. Therefore, you should highlight just 10 rows of data in the import wizard - before clicking the **Next** button. The highlighted 10 rows are then automatically loaded into the **Table Tool** (Figure D.102).

Specified Time (d)	N/A	Calculated Value (Bq)	Measurement Time (d)	N/A	Measurement Value (Bq)	Data Type	Measurement Error	Error Distribution	Theoretical Value (Bq)	Chi-Square
1			7.000E+00		4.98750E+05	Real	1.800E+00	LOGNORM		
2			1.400E+01		2.83500E+05	Real	1.800E+00	LOGNORM		
3			2.100E+01		6.95625E+05	Real	1.800E+00	LOGNORM		
4			2.800E+01		5.74875E+05	Real	1.800E+00	LOGNORM		
5			3.500E+01		1.26000E+05	Real	1.800E+00	LOGNORM		
6			4.200E+01		1.12875E+05	Real	1.800E+00	LOGNORM		
7			4.900E+01		9.4500E+04	Real	1.800E+00	LOGNORM		
8			5.600E+01		4.7250E+04	Real	1.800E+00	LOGNORM		
9			6.300E+01		8.6625E+04	Real	1.800E+00	LOGNORM		
10			7.000E+01		8.4000E+04	Real	1.800E+00	LOGNORM		

Figure D.102. 10 rows of bioassay (whole body) data imported into the **Table Tool**.

Clicking "OK" in the **Table Tool** returns you to the **Bioassay Calculations** screen - with the **Tritium Routine Monitoring Tool** window still open. However, the imported data is now visible (automatically) in this window (Figure D.103).

Tritium Routine Monitoring Tool

File Tools Help

Chemical Form

☒ inorganic H (HTO)
☐ organic H (HCT)

Intakes

Number of Intake Regimes (IRs) to use in the calculation: 10 Intake assumption: ☒ Single acute at midpoint of period
☐ Constant chronic throughout period

Specify the monitoring period corresponding to each measurement

	Monitoring Periods		Measurement Data (Whole Body)		Intake (Bq)
	Start (day)	End (day)	Time (day)	Value (Bq)	
IR 1			7.000E+00	4.96750E+05	1.0000E+00
IR 2			1.400E+01	2.83500E+05	0.0000E+00
IR 3			2.100E+01	6.95625E+05	0.0000E+00
IR 4			2.800E+01	5.74875E+05	0.0000E+00
IR 5			3.500E+01	1.26000E+05	0.0000E+00
IR 6			4.200E+01	1.12875E+05	0.0000E+00
IR 7			4.900E+01	9.4500E+04	0.0000E+00
IR 8			5.600E+01	4.7250E+04	0.0000E+00
IR 9			6.300E+01	8.6625E+04	0.0000E+00
IR 10			7.000E+01	8.4000E+04	0.0000E+00

Default Monitoring Periods Edit Measurement Data

Clear Monitoring Periods

Calc Intakes ..

OK Cancel

Figure D.103. Tritium Routine Monitoring Tool window showing 10 rows of imported data.

The next step is to "Specify the monitoring period corresponding to each measurement". If the sampling intervals are *contiguous*, the associated monitoring periods can be specified automatically - by simply clicking the "Default Monitoring Periods" button (as in Figure D.104).

Tritium Routine Monitoring Tool

File Tools Help

Chemical Form

☒ inorganic H (HTO)
☐ organic H (HCT)

Intakes

Number of Intake Regimes (IRs) to use in the calculation: 10 Intake assumption: ☒ Single acute at midpoint of period
☐ Constant chronic throughout period

Specify the monitoring period corresponding to each measurement

	Monitoring Periods		Measurement Data (Whole Body)		Intake (Bq)
	Start (day)	End (day)	Time (day)	Value (Bq)	
IR 1	0	7.000E+00	7.000E+00	4.96750E+05	1.0000E+00
IR 2	7.000E+00	1.400E+01	1.400E+01	2.83500E+05	0.0000E+00
IR 3	1.400E+01	2.100E+01	2.100E+01	6.95625E+05	0.0000E+00
IR 4	2.100E+01	2.800E+01	2.800E+01	5.74875E+05	0.0000E+00
IR 5	2.800E+01	3.500E+01	3.500E+01	1.26000E+05	0.0000E+00
IR 6	3.500E+01	4.200E+01	4.200E+01	1.12875E+05	0.0000E+00
IR 7	4.200E+01	4.900E+01	4.900E+01	9.4500E+04	0.0000E+00
IR 8	4.900E+01	5.600E+01	5.600E+01	4.7250E+04	0.0000E+00
IR 9	5.600E+01	6.300E+01	6.300E+01	8.6625E+04	0.0000E+00
IR 10	6.300E+01	7.000E+01	7.000E+01	8.4000E+04	0.0000E+00

Default Monitoring Periods Edit Measurement Data

Clear Monitoring Periods

Calc Intakes ..

OK Cancel

Figure D.104. Specifying the monitoring periods automatically.

If the monitoring periods are not in fact all contiguous, you can edit any "Start (day)" value directly in the *Tritium Routine Monitoring Tool* table. Also, clicking the **"Edit Measurement Data"** button (Figure D.104) will return you to the **Table Tool** - so that you can *edit* any of the "input" bioassay data values. The functioning of the *Tritium Routine Monitoring Tool* is integrated with that of the **Table Tool**.

	Warning: By default, the <i>Tritium Routine Monitoring Tool</i> assumes a "Start (day)" value of "0" - since the actual value is not included in the imported data. If "0" is incorrect, you will have to <i>enter</i> the appropriate value yourself. This is generally the "End (day)" of previous (most recent) set of monitoring data.
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D.6.10. Automated Fitting of Tritium Intakes

Once you have loaded a series of up to 10 bioassay results (*i.e.*, 10 rows in the **Measurement Data** table) and defined all of the associated **Monitoring Periods** (as in Figure D.104), you can use the **Tritium Routine Monitoring Tool** to calculate automatically a set of discrete **Intakes** that "fit" the measured bioassay values. In order to do this, you must first assume a value of the "time" of occurrence of each intake. The **Tritium Routine Monitoring Tool** provides two standard (commonly made) assumptions - that are applied automatically to all potential intakes:

- **Single Acute** intake at the *mid-point* of each monitoring period - set by default.
- **Constant Chronic** intake *throughout* each monitoring period.

For the default setting (**Single Acute**), the **Tritium Routine Monitoring Tool** automatically calculates the *time* value corresponding to each sample mid-point. For the **"Constant Chronic"** option, the pre-calculated **"Start (day)"** and **"End (day)"** values are used to calculate the associated Intake values. In order to "fit" the monitoring data (bioassay values), the **Tritium Routine Monitoring Tool** uses the *maximum likelihood method* (as extended to multiple intakes in [IMBA Expert™ OCAS/ORAU-Edition](#)) to find the *most likely* value of the *hypothetical intake* during each sampling period.

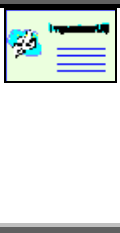
	Important Note #1: In effect, this method in which a limited sequence of monitoring results (maximum of 10) is analyzed does not correct the earliest monitoring results for "carry over" of tritium activity from previous intakes. Thus, the first "calculated" intake amount will always <i>over-estimate</i> the actual intake during this monitoring period - by the amount of "carry over". However this effect will become <i>smaller</i> for each subsequent intake calculation, <i>i.e.</i>, later intakes will be calculated more accurately.
	Important Note #2: This methodology leads to a somewhat <i>conservative</i> estimate of the <i>effective dose</i> committed over the whole monitoring period - although, <i>usually not</i> a <i>serious over-estimate</i> if the whole monitoring period is greater than a month.

Figure D.105 shows the calculated values of intake (**IR1** through **IR10**) that result for the first 10 bioassay measurements (values of whole body activity) in this example. In this case, we have assumed (by default) that each potential intake would have occurred at the mid-point of each sampling period.

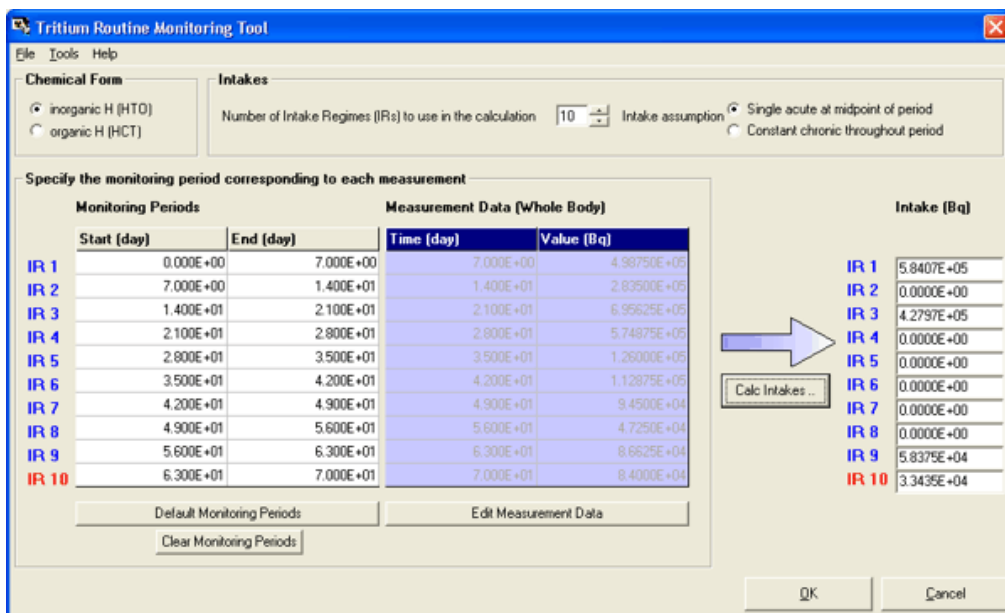


Figure D.105. Result of clicking the "Calc Intakes .." button in the Tritium Routine Monitoring Tool.

Note: For this set of 10 bioassay values, the Tritium Routine Monitoring Tool calculated 4 finite values of intake (for **IR1**, **IR3**, **IR9** and **IR10**). All other potential intakes were calculated to be **zero**.

Clicking the "OK" button in the Tritium Routine Monitoring Tool returns you to the Bioassay Calculations screen (Figure D.106).

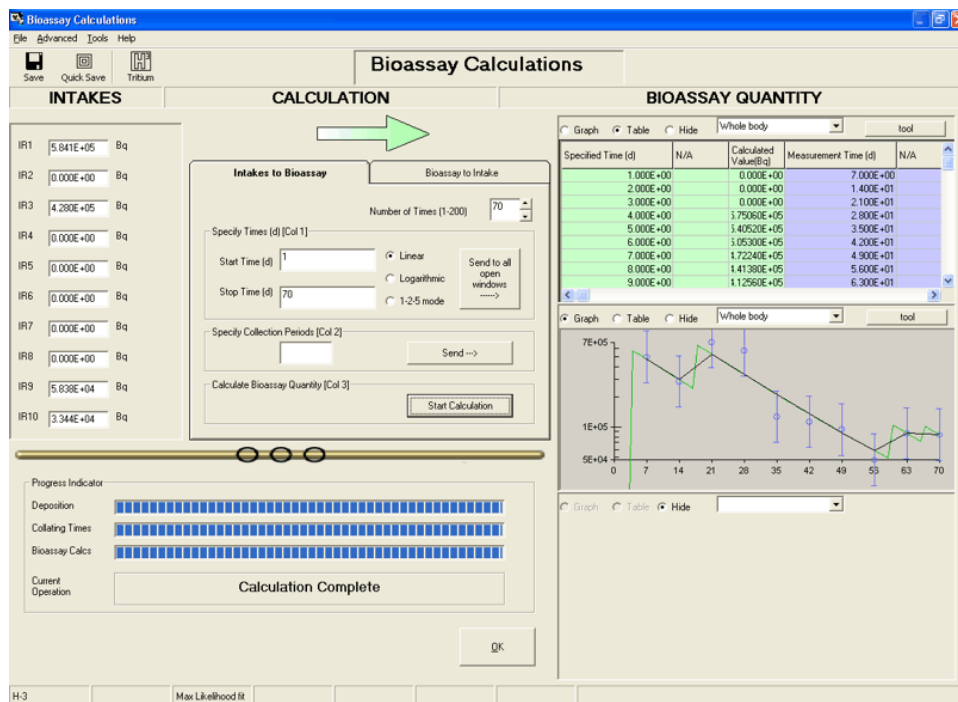


Figure D.106. The amount of intake calculated to have given rise to each successive bioassay measurement is displayed automatically in the Bioassay Calculations screen.



Tip: If you set up a **Graph** window for the **Bioassay Quantity** (Figure D.106), you can view (automatically) the result of the fitting process - in this example, the fitted whole body retention as a function of time together with the input "point estimates" represented by the measured (bioassay) values.



Note: The fitted whole body retention shown in Figure D.106 results from assuming that each of the 4 fitted intakes occurred at the mid-point of the corresponding sampling interval. The effect of the alternative assumption (that each intake occurred continuously over the corresponding sampling interval) is described in Section D.6.12 ("Effect of Assumed HTO Intake Pattern").

Clicking "OK" in the **Bioassay Calculations** screen then returns you to the Main Screen (Figure D.107).

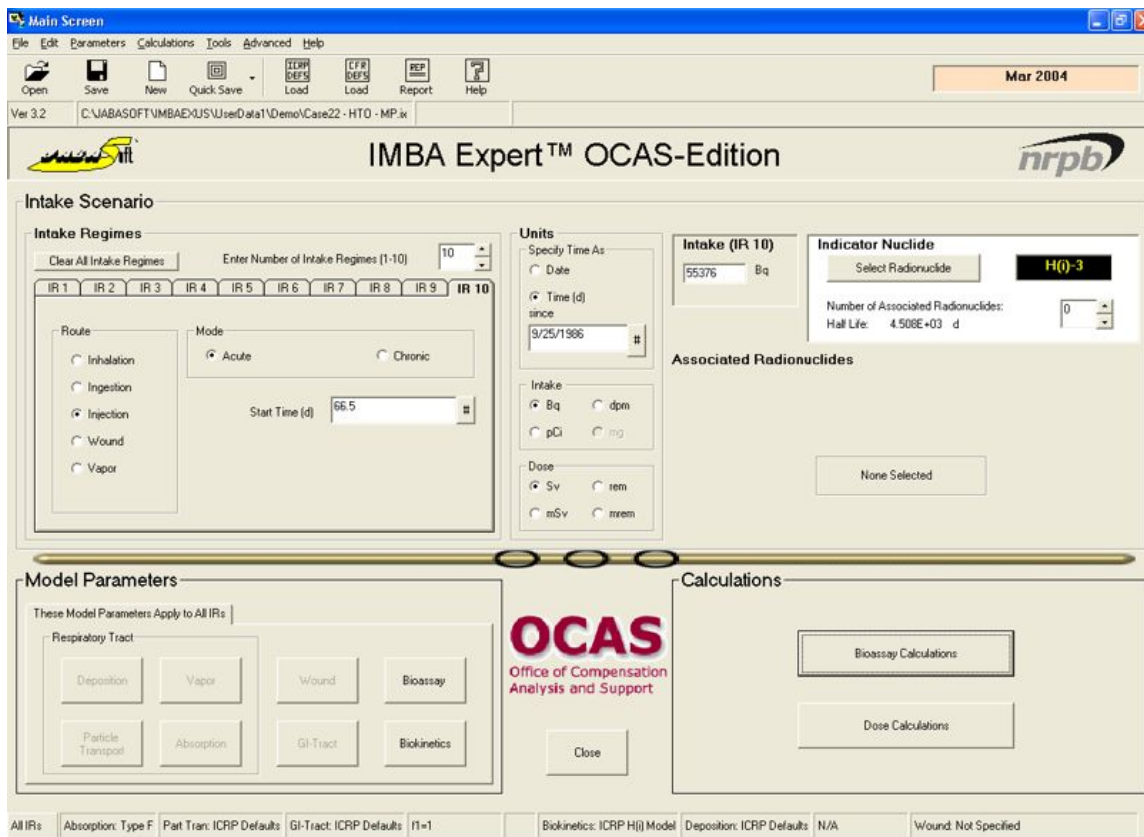


Figure D.107. Main Screen after returning from the **Tritium Routine Monitoring Tool**.



Note: The calculated intake values (and the assumed times and durations of the intakes) are automatically displayed in the **Main Screen** - so that you can proceed directly to the **Dose Calculation**.

D.6.11. Automated Tritium Dose Calculation

Clicking the **Dose Calculations** button in the **Main Screen** opens the **Dose Calculations** screen (Figure D.108). Then, to calculate the resulting values of effective dose, you simply *click* the "**Calculate**" button. The results for the whole tritium monitoring period (**0 to 70 d**) are shown in Figure D.108.

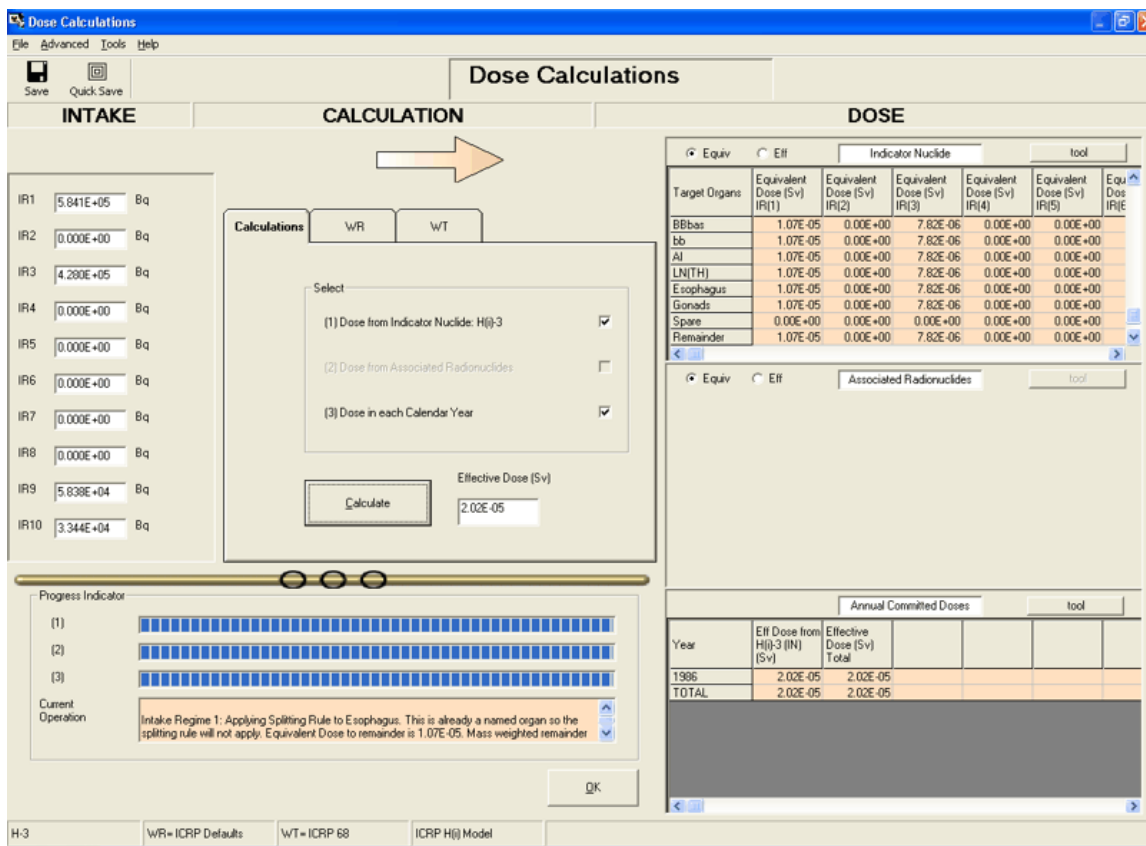


Figure D.108. Calculating and displaying the resulting committed effective dose.

In this case, the *total committed effective dose* is **20.2 μ Sv**. Repeating this whole process for subsequent sets of 10 tritium monitoring results - by importing rows of data 10-at-a-time from the ASCII text file "**Case_22_Tritium.txt**" - gives the calculated values of committed effective dose shown in Table D.8.

Note: There are 65 rows of data, imported as 6 sets of 10 values with a residual set of 5 values.

Table D.8. Total committed effective dose calculated for each monitoring period.

Monitoring period (d)	Total Committed Effective Dose (μSv)
#1: 0 - 70	20.2
#2: 70 - 161	4.6
#3: 161 - 259	8.7
#4: 259 - 343	57.6
#5: 343 - 427	179
#6: 427 - 518	43.6
#7: 518 - 553	3.5
Total: 0 - 553	317

Note: These calculated values assume that intakes occurred at the mid-point of the corresponding sampling interval. The total committed effective dose (**317 μSv**) is *substantially lower* than the value (**479 μSv**) calculated earlier - by manually "fitting" discrete intake events to the whole bioassay data set.

D.6.12. Effect of Assumed HTO Intake Pattern

Instead of using the default assumption that all intakes occur at the *mid-point* of the corresponding sampling period, the **Tritium Routine Monitoring Tool** gives you the option of assuming that all intakes occur continuously (i.e., are uniform chronic) over the corresponding sampling interval. Figure D.109 shows the effect of making the *uniform chronic* assumption on the intakes calculated for the first set of monitoring data (from 0 to 70d).

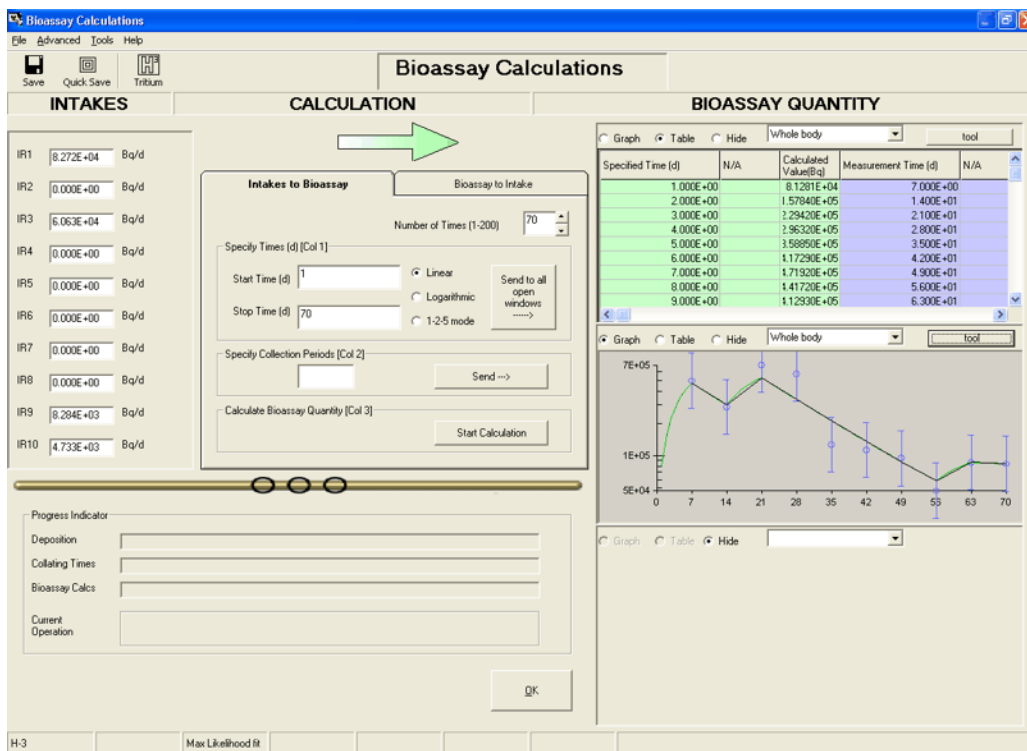


Figure D.109. The amount of intake calculated to have given rise to each successive bioassay measurement on the assumption of constant chronic intake over the corresponding sampling interval.

The resulting values of committed effective dose calculated for all 7 monitoring periods in this example (assuming constant chronic intake over the corresponding sampling interval) are shown in Table D.9.

Table D.9. Total committed effective doses calculated for each monitoring period.

Monitoring period (d)	Total Committed Effective Dose (μSv)
#1: 0 - 70	20.0
#2: 70 - 161	4.5
#3: 161 - 259	8.3
#4: 259 - 343	57.0
#5: 343 - 427	177
#6: 427 - 518	43.1
#7: 518 - 553	3.4
Total: 0 - 553	313



Note: These calculated values are very close to (*marginally lower* than) the values calculated by assuming that the intakes occurred at the mid-point of the corresponding sampling interval. The total committed effective dose is (**313 μSv**) - to be compared with (**317 μSv**) for the "mid-point" assumption (Table D.8).

D.6.13. Automated vs. Manual HTO Analysis

In this section we:

- Test the repeatability of the manual "fitting" procedure.
- Examine the effect of using < 10 sampling intervals in the "automated" procedure.
- Compare the "goodness of fit" of the "manual" and "automated" procedures.

1. Repeatability of "Manual" Fitting

The parameter file "**Case22 - HTO - JA.ix**" contains a solution to this example case that was obtained (by ACJ & Associates, Inc.) independently of the "**Case22 - HTO - MP.ix**" solution. This independent solution is shown in Figure D.110.

Table D.9 shows the 10 discrete intakes fitted to the bioassay data - *c.f.*, the results of the earlier solution (Table D.7). Comparison of the values in Table D.9 with those in Table D.7 shows substantial differences. However, it is more difficult to detect (by eye) substantial differences (biasses?) in the graphical displays of the corresponding data fits - Figure D.110 vs Figure D.92, respectively.

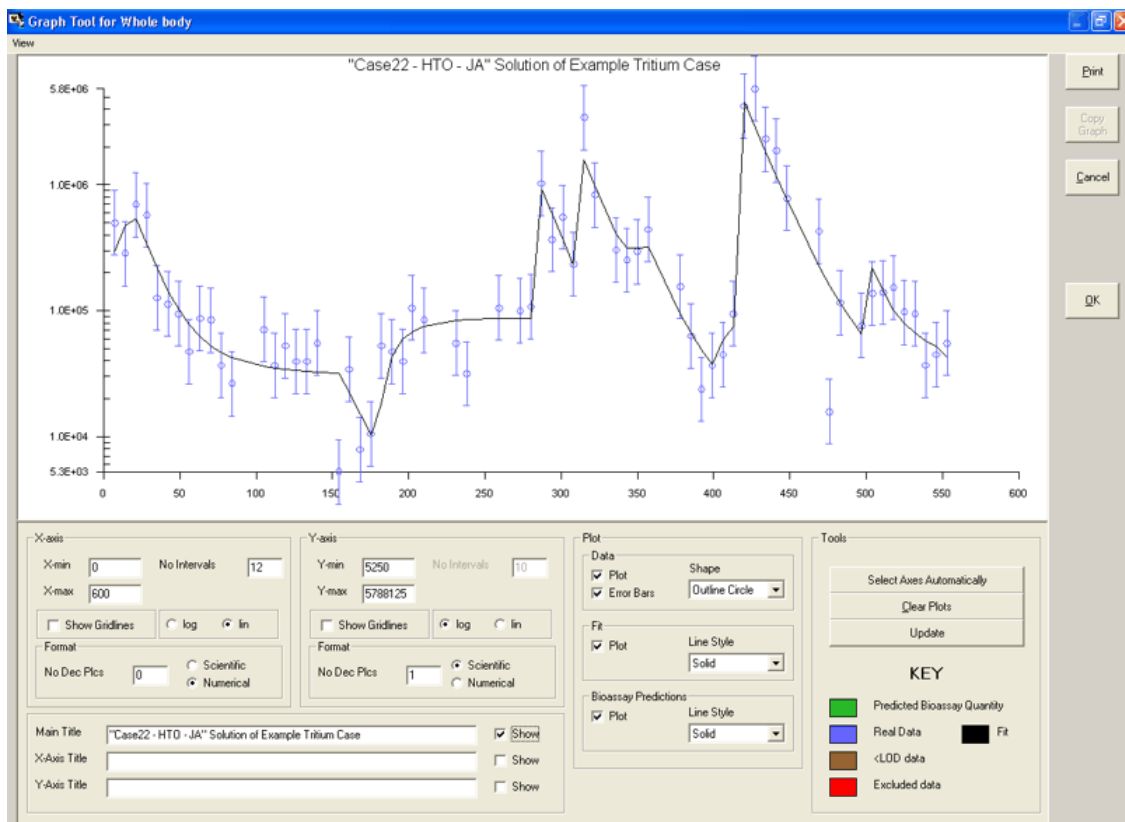


Figure D.110. A second solution of the tritium routine monitoring example case.

Table D.10. Discrete intake calculated from the tritium urinalysis data.

Intake regime	Assumed timing	Intake amount/rate (Bq/Bq d ⁻¹)
IR1 - chronic	0 - 20 d	51,330 Bq/d
IR2 - chronic	40 - 155 d	1,860 Bq/d
IR3 - chronic	180 - 280 d	5,495 Bq/d
IR4 – acute	280 d	1,354,000 Bq
IR5 – acute	310 d	1,940,000 Bq
IR6 - chronic	340 - 357 d	61,810 Bq/d
IR7 - chronic	400 - 440 d	5,837 Bq/d
IR8 – acute	418 d	4,977,000 Bq
IR9 – acute	500 d	213,700 Bq
IR10 - chronic	520 - 550 d	1,654 Bq/d

Figure D.111 shows the committed effective doses calculated from the estimates of intake given in Table D.10.

Note #1: The total committed effective dose calculated in this second solution (**199 μ Sv**) is *less than half* the value (**479 μ Sv**) calculated in the earlier solution.

Note #2: However, the *average* of the two independent estimates of total committed effective dose is **339 μ Sv ($\pm 198 \mu$ Sv standard deviation)**. This is within **8%** of the average value (**315 μ Sv**) obtained using the "automated" fitting procedure!

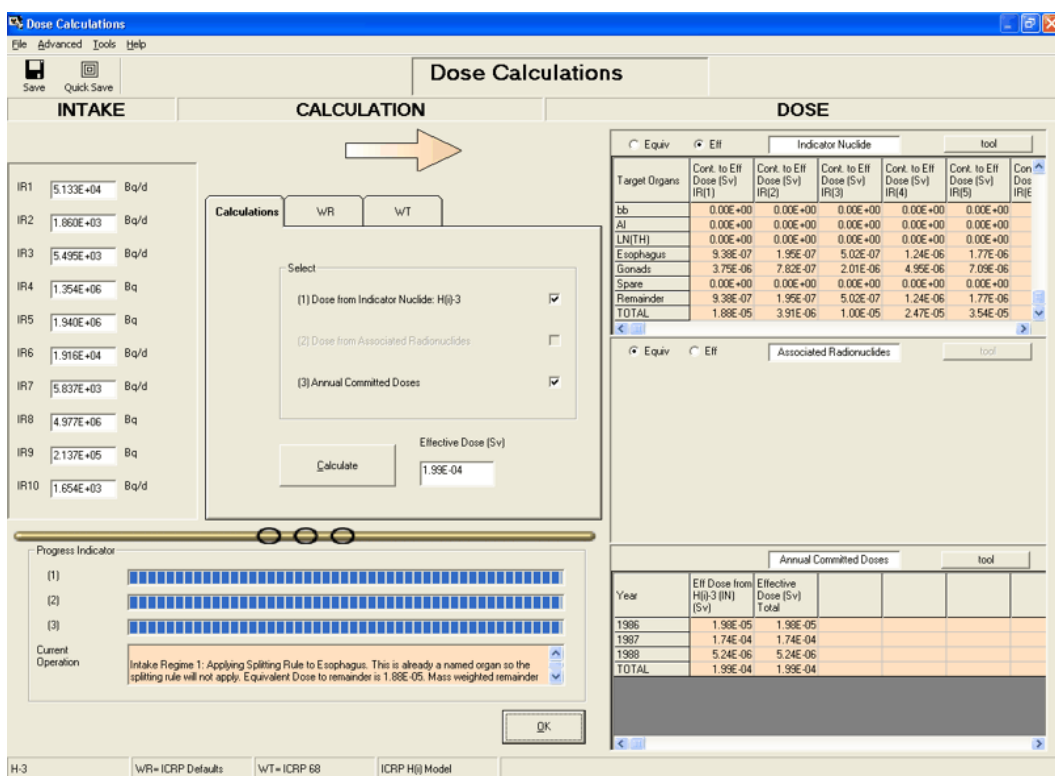


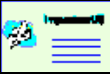
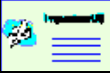
Figure D.111. Dose calculated from the second solution of the tritium routine monitoring example case.

2. Effect of using Fewer Sampling Intervals in the "Automated" Procedure

In order to examine the effect of using fewer sampling intervals in the automated analysis, we repeated the Automated Tritium Intake Estimation (and Dose Calculation) using 13 sets of 5 measured values (rows of data) - instead of 6 sets of 10 values plus a residual set of 5 values. The resulting calculated doses are shown in Table D.11. They are to be compared with those shown in Table D.9 (where the monitoring period was divided into seven parts). In both cases, it was assumed that intakes occurred at the *mid-point* of the corresponding sampling interval.

Table D.11. Total committed effective dose calculated for each monitoring period.

Total Committed Effective Dose	
Monitoring period (d)	(μ Sv)
#1: 0 - 35	19.9
#2: 35 - 70	4.7
#3: 70 - 119	3.6
#4: 119 - 161	1.9
#5: 161 - 196	1.9
#6: 196 - 259	7.4
#7: 259 - 301	25.5
#8: 301 - 343	40.9
#9: 343 - 392	11.3
#10: 392 - 427	168
#11: 427 - 476	37.7
#12: 476 - 259	8.2
#13: 518 - 518	3.5
Total: 0 - 553	334

	Note #1: The total committed effective dose (334 μSv) shown in Table D.11 is <i>higher</i> (by 5%) than the value (317 μSv) obtained earlier - when we analyzed larger sets ($6 \times 10 + 1 \times 5$) of bioassay data.
	Note #2: This observation is consistent with our earlier Important Note that the analysis of a small series of tritium sample values tends to <i>over-estimate</i> the total intake (and thus dose). If previous intake has occurred (within a month-or-so), the value of intake calculated for the first sampling interval of a new set will ALWAYS over-estimate the actual intake value (assuming no bias in the "time of intake" model, since there will always be some "carry-over" of tritium activity from the previous intake. The amount of this "un-corrected" carry-over decreases with each subsequent sample. Therefore, the more sample values included in the set, the <i>smaller</i> the resulting <i>over-estimate for the set as a whole</i> . It follows that the earlier analysis (using the maximum number of sample values in each set) should have given a <i>less biased</i> estimate of total intake (and committed dose) than this analysis carried out with only 5 sample values in each set.

3. "Goodness of Fit" Comparison between "Automated" and "Manual" Procedures

Table D.12 summarizes the estimates of effective dose committed over the whole (553-d) monitoring period - comparing the results of both manual fitting exercises and both "automated" fits. The table also shows the total value of χ^2 calculated in each case by comparing the "predicted" and "observed" values of the bioassay quantity.

Table D.12. Comparison of estimated total committed doses and the associated χ^2 -sum statistic.

Case Analysis: Intake Assumption	Estimated Effective Dose (μSv)	χ^2 -sum
Manual (Whole Dataset):		
MP	479	56.9
JA	199	55.7
Automated ($6 \times 10 + 1 \times 5$):		
"Mid-point"	317	25.2
"Continuous"	313	25.2
Automated (13×5):		
"Mid-point"	334	24.4
"Continuous"	331	24.4

The points to **note** from Table D.12 are:

- The "Manual" analyses (of the whole dataset) differed only *marginally* in their "goodness of fit" - i.e., the respective χ^2 -sum statistics were 56.9 and 55.7 (for 10 intakes fitted to 65 data points) - and yet the resulting estimates of total committed dose differed by a *large* factor (2.4).
- The "Automated" analyses can (and do) fit a larger number of discrete intakes to the dataset as a whole - thus there are fewer "degrees of freedom" - with the result that the χ^2 values are substantially smaller.
- With these example data (from routine weekly monitoring), the assumed time of occurrence of intake ("mid-point" or "continuous") makes *very little* difference (*less than 2%*) to the calculated values of committed dose - and no overall difference to the χ^2 statistic.

- The (5% lower) value of total committed dose calculated using bioassay values 10-at-a-time (the maximum number) is likely to be *more accurate* (less biased) than value obtained by analyzing bioassay values 5-at-a-time.



Note: This topic should be studied further using Monte Carlo methods to simulate complex tritium intake patterns - and the resulting variability in the bioassay sample values. The applicability and performance of the "Tritium Tool" provided here should thus be examined further.

D.7. ²⁴¹Am Lung Counting (for ²⁴¹Pu)

This case involved an acute inhalation of high-fired plutonium oxide. It is of particular interest because about 94% of the plutonium activity was ²⁴¹Pu (at the time of the inhalation). The ²⁴¹Am progeny of ²⁴¹Pu was present in the inhaled material - with about 0.9% of the total plutonium activity. However, this amount of ²⁴¹Am "contamination" enabled the retention of material in the lungs to be measured relatively accurately - over many years.

The case was first reported in the literature by Bihl et al (1988), with a longer-term "follow-up" reported by Carbaugh et al (1991). These authors concluded that this case demonstrated very unusual respiratory tract clearance behavior, both in terms of low "solubility" of the plutonium particles (evidenced by an undetectable excretion rate in urine), and the virtual absence of particle clearance from the respiratory tract. In fact, Bihl et al coined the term "Super Class Y" to describe the unusually low solubility, and, rather than decreasing over time, the ²⁴¹Am activity in the lungs actually built up - by a factor of about 2 - over 12 years.

Very recently (January 28th, 2004), Gene Carbaugh (PNNL) has published an updated slide presentation on this case - entitled 'The Plutonium Reality Show: "Super Class Y vs. Class W and Class Y" - A Contest of Bioassay and Internal Dosimetry'² - We have taken an exploratory look at this case (HAN-1) here.

The raw data (provided in an Excel spreadsheet by Gene Carbaugh, PNNL) include:

- Measured isotopic composition of the inhaled material (% by atom) - from mass spectrometry.
- Measured ²⁴¹Am-in-lung activity *in vivo* - from the first through 6,639th day (18-y follow-up).
- Measured ²⁴¹Am-in-liver activity *in-vivo* - measurable from about 6,000 d.
- Measured ²⁴¹Am-in-skeleton activity *in-vivo* - also measurable from about 6,000 d.
- Measured ^{239/240}Pu excretion rate in urine - measurable from about 1,800 d onwards.

² http://bidug.pnl.gov/references/Carbaugh_PNNL_%20Plutonium_%20Reality_%20Show_s.pdf.

D.7.1. Input Data

1. Isotopic Composition

Table D.13. Isotopic composition of plutonium oxide material inhaled in HAN-1.

Radionuclide	% by Number of atoms	% By Activity
²⁴¹ Am	0.25	0.56
²³⁸ Pu	0.065	0.71
²³⁹ Pu	86.4	3.46
²⁴⁰ Pu	11.6	1.71
²⁴¹ Pu	1.4	93.6
²⁴² Pu	0.24	6×10^{-4}

Clearly, from Table D.13:

- ^{239/240}Pu dominates by number of atoms.
- ²⁴¹Pu dominates by activity.
- ²⁴¹Am is a minor "contaminant" of the plutonium particle "matrix" - in terms of both number of atoms (mass) and activity.

2. ²⁴¹Am in the Lungs

A total of **259** *in vivo* measurements of ²⁴¹Am activity in the lungs. This exceeds the capacity (**200**) for any single Bioassay Quantity provided in [IMBA Expert™ OCAS/ORAU-Edition](#). Therefore, we "reduced" the data set in a manner that would not introduce bias into the fitting procedure - by averaging each successive pair of measurement date and value. The last (odd-numbered) data point was discarded. Table D.14. gives the reduced data set.

Table D.14. Reduced data set of ²⁴¹Am activity in the lungs.

Mid-point Date/Time	Activity (pCi)		
5/23/78 12:00 PM	1300	6/29/79 12:00 AM	1700
5/24/78 12:00 PM	1200	8/13/79 12:00 PM	1600
5/26/78 12:00 AM	1350	10/12/79 12:00 AM	1600
5/30/78 12:00 AM	1300	11/30/79 12:00 AM	1600
6/12/78 12:00 PM	1250	1/25/80 12:00 AM	1600
6/27/78 12:00 AM	1200	3/14/80 12:00 AM	1700
7/10/78 12:00 PM	1200	4/11/80 12:00 AM	1950
7/31/78 12:00 PM	1300	6/13/80 12:00 AM	1750
9/16/78 12:00 PM	1300	9/29/80 12:00 PM	1950
10/11/78 12:00 AM	1500	1/2/81 12:00 AM	1850
11/3/78 12:00 AM	1450	3/16/81 12:00 PM	1700
2/13/79 12:00 PM	1250	5/15/81 12:00 AM	1700
3/14/79 12:00 AM	1450	6/26/81 12:00 AM	1800
4/13/79 12:00 AM	1500	9/23/81 12:00 AM	1650
5/10/79 12:00 PM	1550	1/20/82 12:00 AM	1550
		4/26/82 12:00 PM	1500
		8/13/82 12:00 AM	1750
		12/13/82 12:00 PM	1750

3/28/83 12:00 PM	1950	12/14/90 12:00 AM	2895
7/11/83 12:00 PM	1900	1/11/91 12:00 AM	2880
9/12/83 12:00 PM	2250	2/8/91 12:00 AM	2530
1/13/84 12:00 AM	2650	3/11/91 12:00 PM	2395
2/24/84 12:00 AM	2800	4/29/91 12:00 PM	2595
5/28/84 12:00 PM	3000	6/14/91 12:00 AM	2695
7/27/84 12:00 AM	2550	7/8/91 12:00 PM	2725
10/12/84 12:00 AM	2150	8/30/91 12:00 AM	2345
11/14/84 12:00 PM	2400	9/27/91 12:00 AM	3160
3/11/85 12:00 PM	2500	10/25/91 12:00 AM	2735
5/2/85 12:00 AM	2350	11/22/91 12:00 AM	2490
5/2/85 12:00 AM	2450	12/27/91 12:00 AM	1965
5/2/85 12:00 AM	2300	1/31/92 12:00 AM	3585
7/12/85 12:00 AM	2100	3/27/92 12:00 AM	3395
9/13/85 12:00 AM	2450	4/24/92 12:00 AM	3090
11/25/85 12:00 PM	2500	5/29/92 12:00 AM	3465
3/28/86 12:00 AM	2350	7/31/92 12:00 AM	3300
5/16/86 12:00 AM	2450	8/28/92 12:00 AM	3355
6/27/86 12:00 AM	2375	9/28/92 12:00 PM	2940
8/11/86 12:00 PM	2515	11/9/92 12:00 PM	3225
10/6/86 12:00 PM	2350	12/4/92 12:00 AM	3375
10/17/86 12:00 AM	2445	1/8/93 12:00 AM	3050
12/19/86 12:00 AM	2300	2/12/93 12:00 AM	2930
2/13/87 12:00 AM	2480	3/12/93 12:00 AM	2810
3/27/87 12:00 AM	2600	4/12/93 12:00 PM	3050
6/7/87 12:00 AM	2630	5/14/93 12:00 AM	3105
8/13/87 12:00 PM	2315	6/7/93 12:00 PM	3085
11/12/87 12:00 AM	2975	7/5/93 12:00 PM	2855
11/25/87 12:00 AM	2725	8/23/93 12:00 PM	3325
3/14/88 12:00 PM	2500	10/8/93 12:00 AM	3160
7/11/88 12:00 PM	2335	11/24/93 12:00 PM	3455
9/12/88 12:00 PM	2275	1/12/94 12:00 PM	3160
10/24/88 12:00 PM	2335	2/11/94 12:00 AM	3335
10/24/88 12:00 PM	2335	4/1/94 12:00 AM	2985
12/23/88 12:00 AM	2240	6/10/94 12:00 AM	3480
2/10/89 12:00 AM	2445	7/22/94 12:00 AM	3610
3/10/89 12:00 AM	2060	9/29/94 12:00 AM	3630
4/10/89 12:00 PM	2510	10/13/94 12:00 AM	3630
5/26/89 12:00 AM	2740	11/16/94 12:00 AM	3680
8/4/89 12:00 AM	3375	12/30/94 12:00 AM	3505
8/25/89 12:00 AM	2510	1/27/95 12:00 AM	3390
10/27/89 12:00 AM	2310	2/24/95 12:00 AM	3290
1/26/90 12:00 AM	2840	4/21/95 12:00 AM	3410
3/26/90 12:00 PM	2635	5/19/95 12:00 AM	3145
5/11/90 12:00 AM	2695	6/30/95 12:00 AM	2565
6/11/90 12:00 PM	3130	9/22/95 12:00 AM	4010
7/30/90 12:00 PM	2825	11/3/95 12:00 AM	3390
9/28/90 12:00 AM	2585	4/26/96 12:00 AM	3670
11/12/90 12:00 PM	2760		

3. ²⁴¹Am in the Liver

Table D.15. *In vivo* measurements of ²⁴¹Am activity in the liver.

Date of Measurement	Measured ²⁴¹ Am Activity (nCi)	Minimum Detectable Activity (nCi)
9/29/1994	0.2	0.05
1/27/1995	0.3	0.05
8/25/1995	0.2	0.05
11/17/1995	0.3	0.06
5/31/1996	0.2	0.05
7/26/1996	0.0	0.06

The activity of ²⁴¹Am in the liver was measurable (*in vivo*) from September, 1994 onwards (see Table D.15). To represent these data we have averaged all 6 measured values, and taken this average value (and its standard deviation) to represent the amount of ²⁴¹Am in the liver on September 20th, 1995 (the average of the measurement dates). The resulting "point" estimate is **0.21 ± 0.09 nCi**.

4. ²⁴¹Am in the Skeleton

Table D.16. *In vivo* measurements of ²⁴¹Am activity in the skeleton.

Date of Measurement	Measured ²⁴¹ Am Activity (nCi)	Minimum Detectable Activity (nCi)
7/29/1994	0.0	0.2
12/6/1994	0.4	0.2
5/19/1995	0.2	0.2
3/22/1996	0.2	0.2

The activity of ²⁴¹Am in the skeleton, as measured (*in vivo*) over a similar period to that measured in the liver, is shown in Table D.16. To represent these data we have averaged the 4 measured values, and taken this average (and its standard deviation) to represent the amount of ²⁴¹Am in the skeleton on April 11th, 1995 (the average of the measurement dates). The resulting "point" estimate is **0.20 ± 0.18 nCi**.

5. ²³⁹Pu in Urine

The rate of excretion of ²³⁹Pu in urine was measurable (by ICP mass spectrometry) from 1983 onwards. The calculated activity excretion rates (simulated 24-h urine samples) are shown in Table D.17.

Table D.17. Measured urinary excretion rate of ^{239}Pu .

Measurement	Date of Measured Excretion Rate (pCi d ⁻¹)	Estimated Error (pCi d ⁻¹)
4/20/1983	0.0071	0.0038
12/21/1983	0.0081	0.0041
9/20/1984	0.0090	0.0025
7/11/1985	0.0207	0.0043
7/9/1986	0.0062	0.0021
7/8/1987	0.0017	0.0019
7/12/1988	0.0031	0.0018
7/13/1989	0.0065	0.0035
8/21/1990	0.0059	0.0041
7/11/1991	0.0153	0.0058
7/22/1992	0.0131	0.0034
7/14/1993	0.0194	0.0039
7/20/1994	0.0071	0.0025
7/18/1995	0.0181	0.0038
7/10/1996	0.0179	0.0037

D.7.2. Analysis of ^{241}Am -in-Lung Data – Using ICRP Defaults

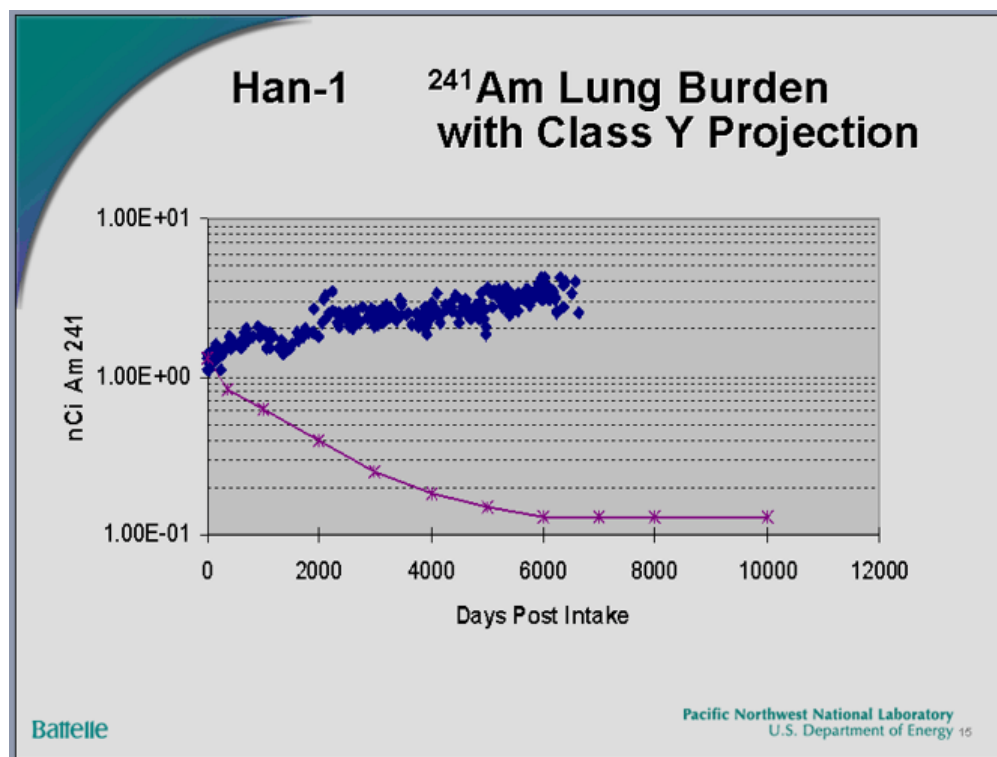


Figure D.112. Comparison of ^{241}Am -in-lung data with ICRP30 Class 'Y' prediction (from Carbaugh 2004).

Figure D.112 shows Gene Carbaugh's updated summary of the ^{241}Am -in-lung data from the HAN-1 case, compared with the temporal behavior "predicted" by the ICRP Publication 30 (ICRP79)

lung model - for Class 'Y' plutonium. Beyond 6,000 d, the measured ^{241}Am retention is about 30-fold greater than predicted.

We have analyzed these data using [IMBA Expert™ OCAS/ORAU-Edition](#) - with the current ICRP "default" assumption of Type 'S' absorption characteristics (Figure D.113). The "fit" is better than for Class 'Y' - but still *very bad*. Figure D.113 also compares the "predicted" build-up of ^{241}Am activity in the **Liver** and **Skeleton** with the *in vivo* measurements.

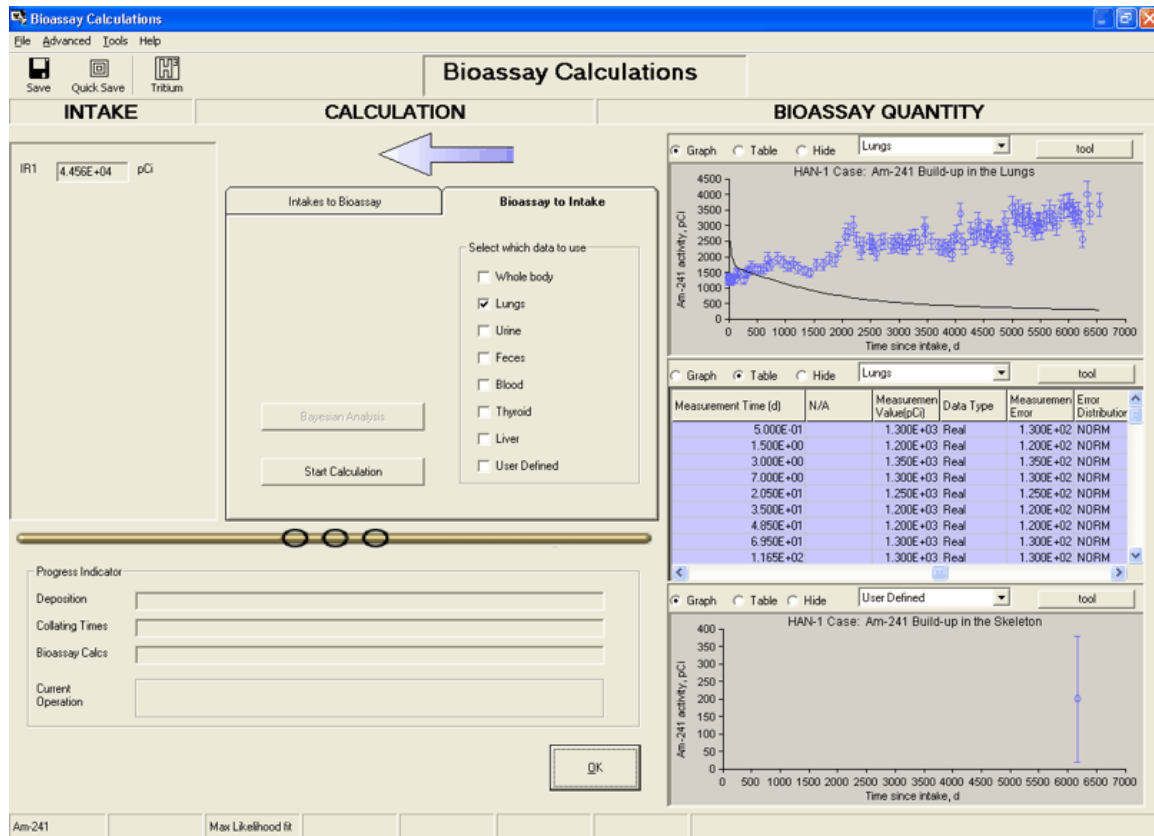


Figure D.113. Most likely "fit" to HAN-1 ^{241}Am -in-lung data assuming ICRP default HRTM parameter values (Type 'S').

Note: The predicted monotonic decrease of ^{241}Am activity in the lung includes the calculated "in-growth" of ^{241}Am activity into that of the parent ^{241}Pu .

In this example, [IMBA Expert™ OCAS/ORAU-Edition](#) automatically calculated the "in-growth" of ^{241}Am activity in the respiratory tract that resulted from the decay of ^{241}Pu . However, in order to do this, it was first necessary to *define* the Isotopic Composition of the inhaled plutonium material. This was done by treating all of the isotopes of plutonium that are present in the particle matrix as Associated Radionuclides of ^{241}Am (the Indicator Nuclide) - see Figure D.114.

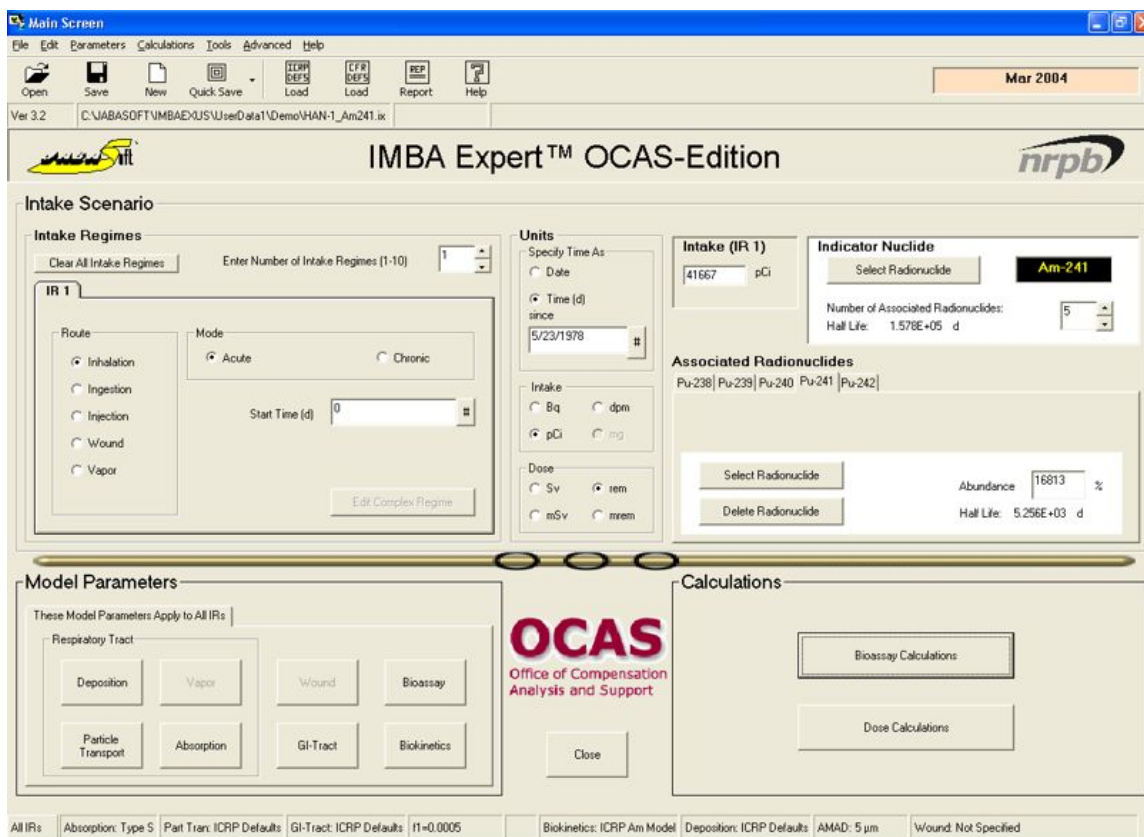


Figure D.114. Setting up plutonium isotopes as **Associated Radionuclides**.

Figure D.114 shows the 5 associated plutonium isotopes - ^{238}Pu , ^{239}Pu , ^{240}Pu , ^{241}Pu and ^{242}Pu . **Note** that the "Abundance" of ^{241}Pu is very high (16,813% - relative to the ^{241}Am activity).

The calculated amount of ^{241}Am intake was **41,691 pCi** - on the assumption that the inhaled plutonium oxide (particle matrix) had Type 'S' absorption behavior. The relative abundance of ^{239}Pu was **621%** (Table D.13). Therefore, the associated intake of ^{239}Pu would have been **258,900 pCi (258.9 nCi)**.

We can test this estimate of the ^{239}Pu intake by comparing the predicted excretion rate in urine with that actually measured (Table D.17). To do this, however, we have to set up a second "case" in **IMBA Expert™ OCAS/ORAU-Edition** - with ^{239}Pu as the Indicator Nuclide, and the amount of intake set at **258,900 pCi**. The resulting "predicted" urinary excretion rate is shown in Figure D.115.

The urinary excretion rate for inhaled Type 'S' plutonium is predicted to *decrease* after about 1,000 d (Figure D.115). However, the trend in the measured values (from about 1,800 through 6,700 d) is for the actual urinary excretion rate to *increase* with time. Again, therefore, the "fit" to the observed temporal behavior of urinary excretion (of ^{239}Pu) is *not good*.

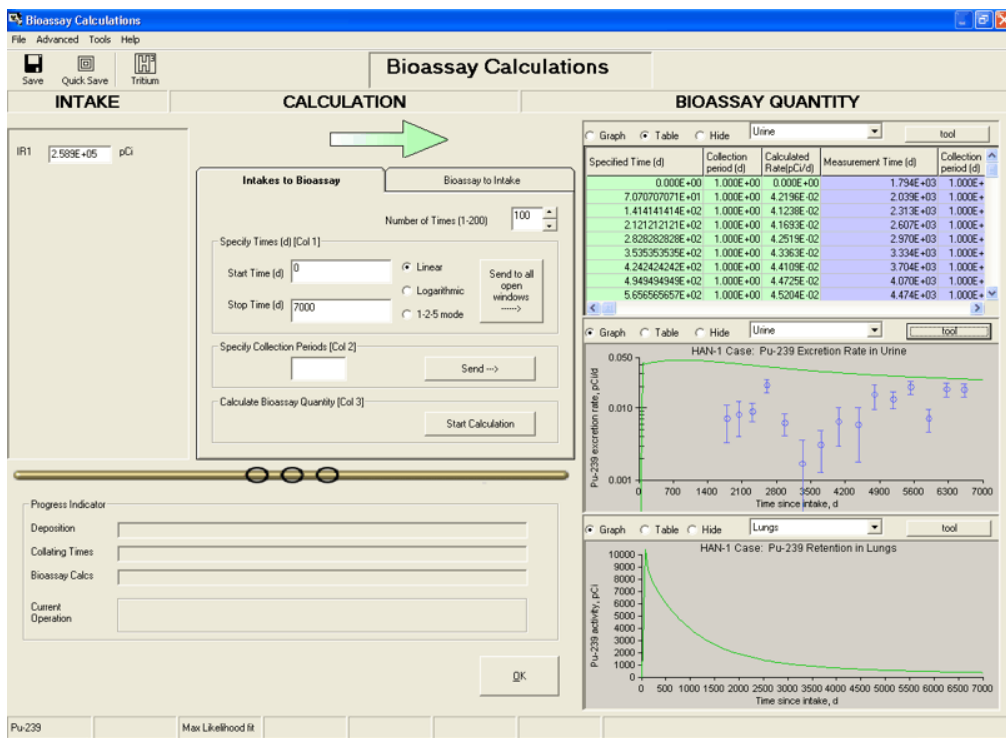


Figure D.115. Urinary excretion rate and lung retention predicted for Type 'S' plutonium.

Summary of Observed Departures from ICRP-Default Behavior

The following observations are NOT consistent with the predictions (for a particle matrix consisting of Type 'S' plutonium):

1. The the measured ²⁴¹Am activity in the lungs remained essentially constant over the first 70 d (Figure D.116) - whereas Type 'S' absorption together with ICRP's recommended mechanical transport rates from the alveolar-interstitial (AI) region predicted a marked *decrease* of activity over this initial period (Figure D.116). Note that the effect of "in-growth" of ²⁴¹Am activity as a result of ²⁴¹Pu decay over this period is *negligible*.
2. Over the long term (18 y) the ²⁴¹Am activity in the lungs was observed to *increase* markedly - whereas, for Type 'S' plutonium it should have *decreased* approximately 10-fold (Figure D.113).

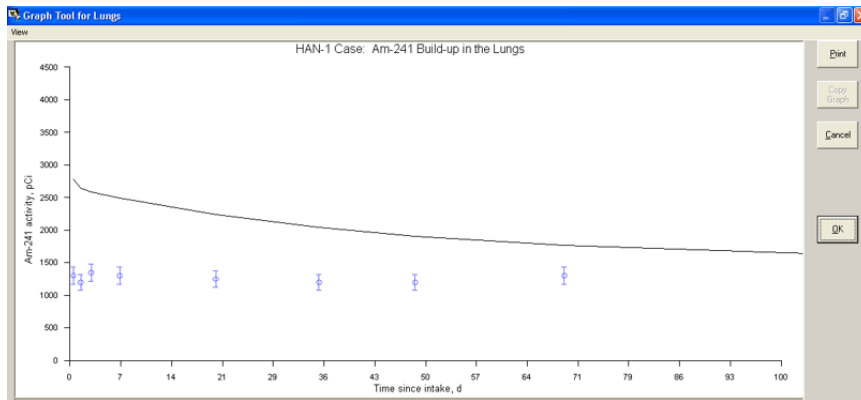


Figure D.116. Comparison of predicted and measured early changes in ²⁴¹Am activity in the lungs.

From the above, it appears that BOTH the *absorption characteristics* of the plutonium particle matrix AND the *mechanical elimination rate* of particles deposited in the "deep lung" of this *individual worker* differ substantially from the standard ICRP **default** values.



Note: ICRP has recommended that **Default** parameter values should be used *in the absence of better (specific) information*. This case is a prime example of significant departure in parameterized characteristics from the available defaults.

D.7.3. Optimizing HRTM Parameter Values to Fit HAN-1 Data

In order to obtain a credible "fit" to ALL of the **HAN-1** data, we found it necessary to vary the following parameter values:

1. In the **HRTM Mechanical Transport Model** (Figure D.117) - the *rates of transport* to the bronchioles (compartments bb_1) from BOTH compartments Al_1 and Al_2 (of the alveolar-interstitial region).
2. In the **HRTM Particle Absorption Model** (Figure D.118) - the "*slow*" *absorption rate*.
3. In the **HRTM Particle Deposition Model** (Figure D.119) - the *aerosol AMAD*.

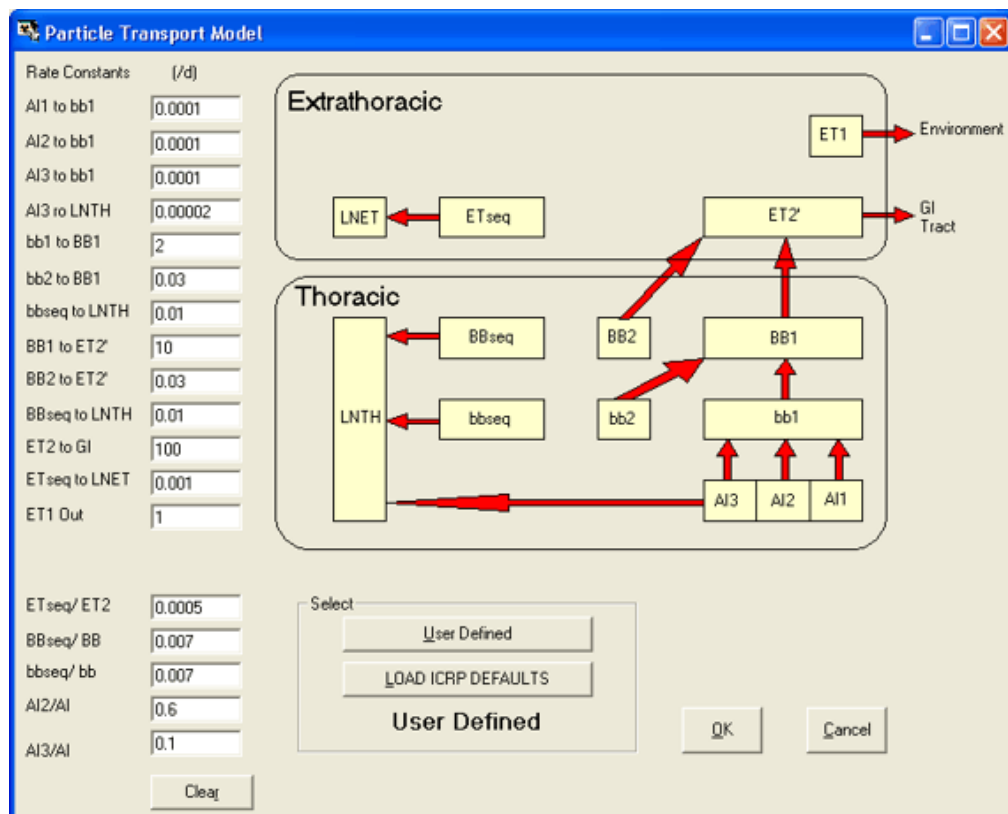


Figure D.117. User Defined values of the Rate Constants "Al1 to bb1" and "Al2 to bb2" - from their default values of " 0.02 d^{-1} " and " 0.001 d^{-1} ", respectively.

These changes to the transport rates out of compartments AI_1 and AI_2 are equivalent to *eliminating* the "fast" and "intermediate" phases of mechanical particle clearance from the AI region. In other words, ALL of the material deposited in the AI region is cleared "slowly" - at the ICRP-recommended rate for "slow" clearance. Such clearance behavior has been observed previously in some individuals (ICRP 1994a) - and is not uncommon in cigarette smokers.

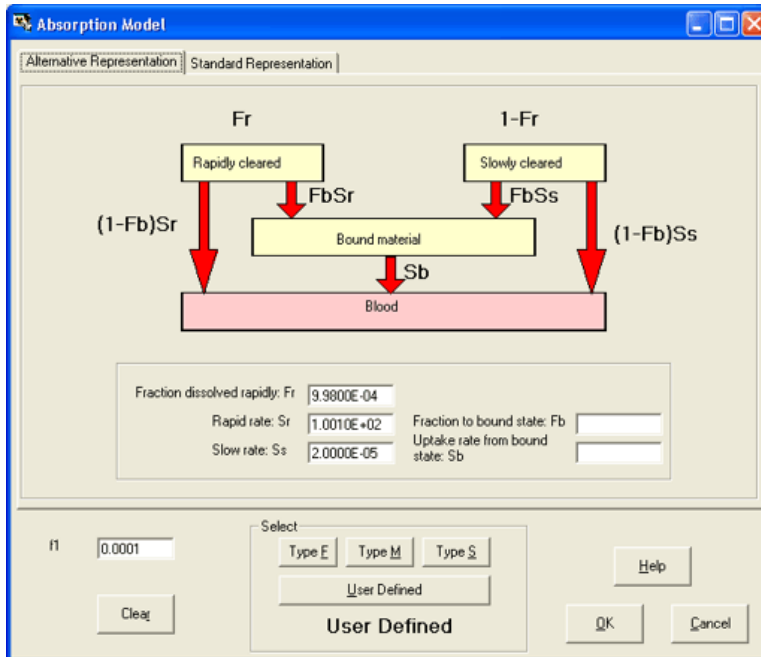


Figure D.118. User Defined value of the "Slow" absorption rate (S_s) - from the default value of 0.0001 d^{-1} for Type 'S'.

This changed "slow" absorption rate (S_s) represents a *five-fold reduction* from the Type 'S' default values (0.0001 d^{-1}).

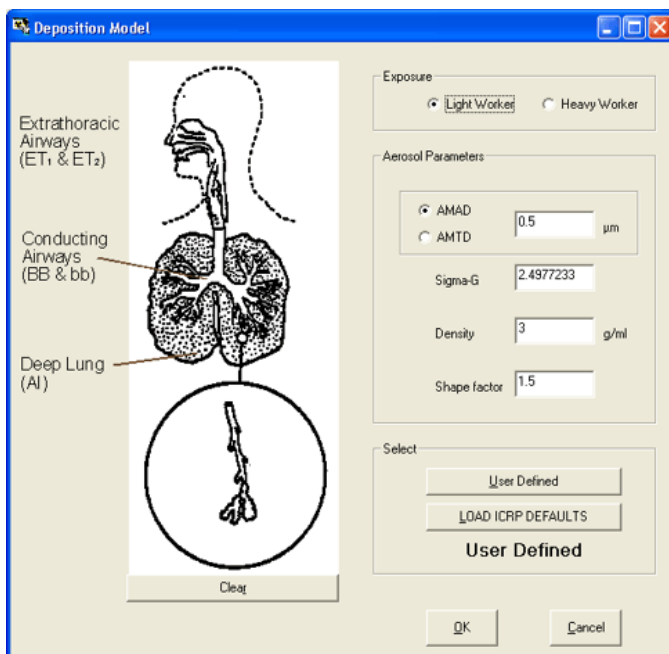


Figure D.119. User Defined value of the aerosol AMAD ($0.5 \mu\text{m}$).

	Tip #1: The parameter files " HAN-1_Am-241.ix " and " HAN-1_Pu-239.ix ", for ^{241}Am and ^{239}Pu as the Indicator Nuclide , respectively, have been set up with these modified parameter values - together with the HAN-1 "test" data.
	Tip #2: It is informative to try varying these parameter values - so as to understand the effect of each one on the overall "fit" to these data. You will find that the "appropriate" range of parameter values is reasonably tightly defined.

D.7.4. Improved Representation of the HAN-1 Data

Figure D.120 shows the resulting improved "fit" to the measured build-up of ^{241}Am activity in the lungs. Furthermore, Figure D.121 shows that the very much improved "fit" to the observed early "constancy" of the ^{241}Am activity in the lungs.

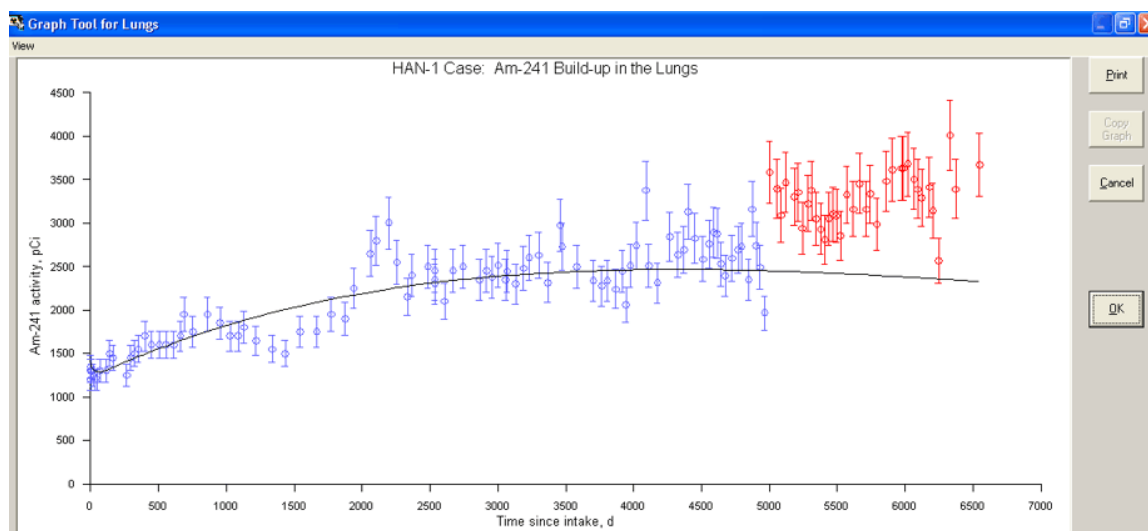


Figure D.120. Improved "fit" to the measured **build-up** of ^{241}Am activity in the lungs.

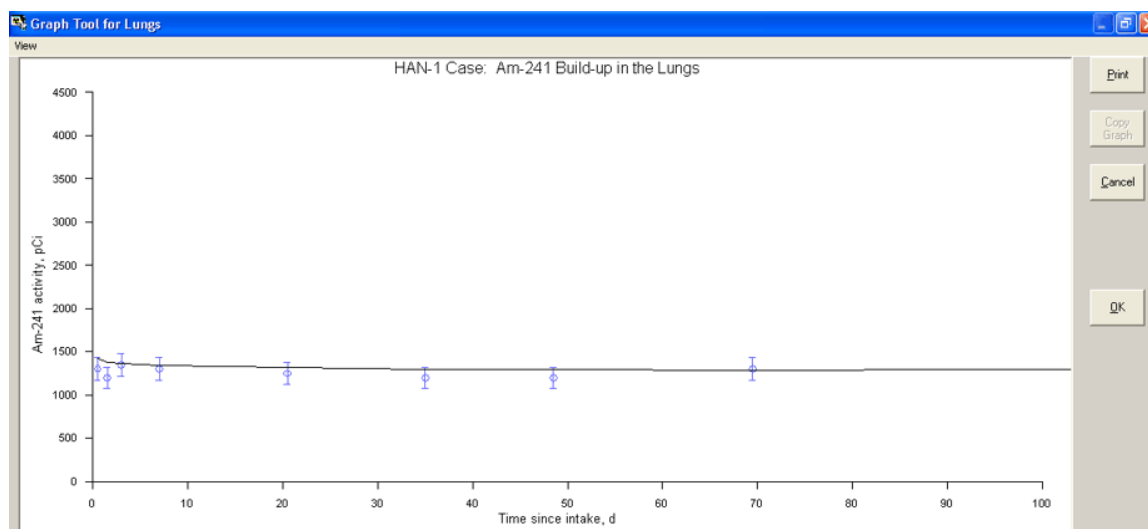


Figure D.121. Resulting "fit" to constant ^{241}Am activity in the lungs measured over the first 70 d.

You will have noted (from Figure D.120) that we have *excluded* from this "fit" the last "block" of data (from about 5,000 d onwards). There is clearly a "discontinuity" in the measured values at about 5,000 d. By excluding these data, we have obtained a better overall "fit".



Tip: See for yourself how *inclusion/exclusion* of the last "block" of data affects the overall "fit". You will find that the effect is not unduly critical!

Figure D.122 includes the "predicted" build-up of ^{241}Am activity in the **Liver** and **Skeleton**.

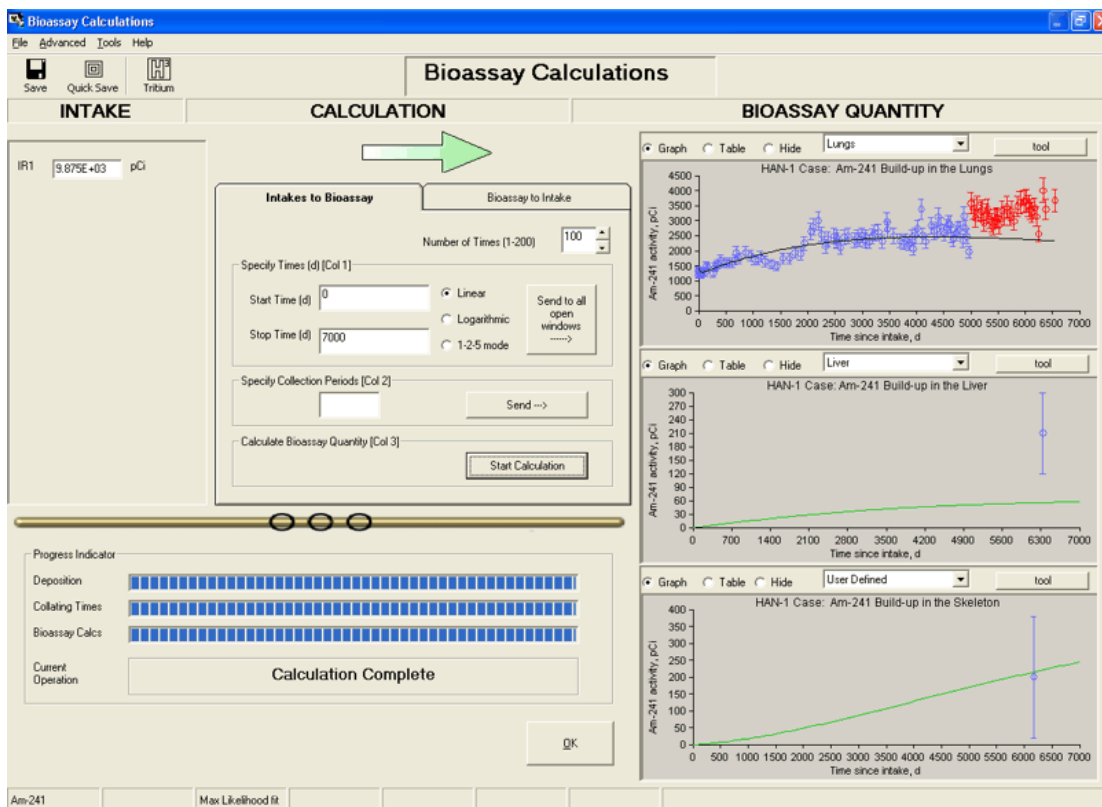


Figure D.122. Improved overall "fit" to the HAN-1 data obtained by modifying parameter values in the HRTM.



Important Note: The calculated build-up of ^{241}Am activity in the **Liver** and **Skeleton** does NOT include "in-growth" from ^{241}Pu that is also taken up by these organs. **IMBA Expert™ OCAS/ORAU-Edition** calculates such "in-growth" ONLY for the lungs - where it is assumed that ^{241}Am formed from decay of ^{241}Pu in the particle matrix remains with the plutonium "bulk" material. For the **Associated Radionuclides** in body organs, including ^{241}Pu , progeny "in-growth" is calculated ONLY as part of the **Dose Calculation**.



Note: **Skeletal Retention** is NOT one of the 7 "explicit" **Bioassay Quantities** in **IMBA Expert™ OCAS/ORAU-Edition**. However, the "User Defined" quantity can be set up (with the appropriate bioassay function) to represent skeletal retention. **Appendix A: Technical Basis** includes a suitable bioassay function for americium retention in the skeleton. This is already implemented in the parameter file "**HAN-1_Am-241.ix**".

Figure D.123 shows the resulting "fit" to the ^{239}Pu excretion rate in urine. this is a substantially more "credible" representation of the measured values than the initial "prediction" - based on ICRP default parameter values (Figure D.115).

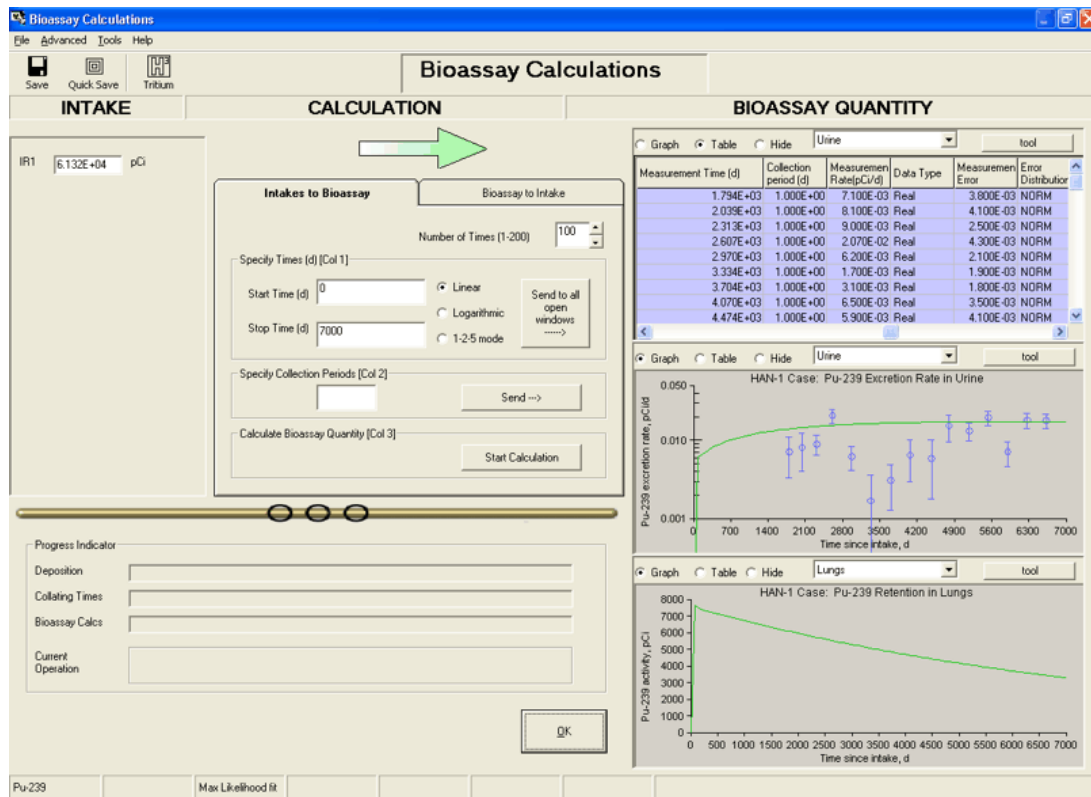


Figure D.123. Predicted ^{239}Pu urinary excretion rate and lung retention.

Note: As with the other example cases "solved" in this **User Manual**, the "solutions" offered are NOT intended to be scientifically definitive. They are presented ONLY to demonstrate the scope and flexibility of the **IMBA Expert™ OCAS/ORAU-Edition**. More thorough review of the specific health physics information relating to each case may well indicate revised modeling assumptions.

D.7.5. Dose Calculation for HAN-1 Case

We can use EITHER the "HAN-1_Pu-239.ix" OR the "HAN-1_Am-241.ix" parameter file to calculate the resulting committed effective doses - so we will use BOTH - with the **10CFR835** tissue weighting factors.

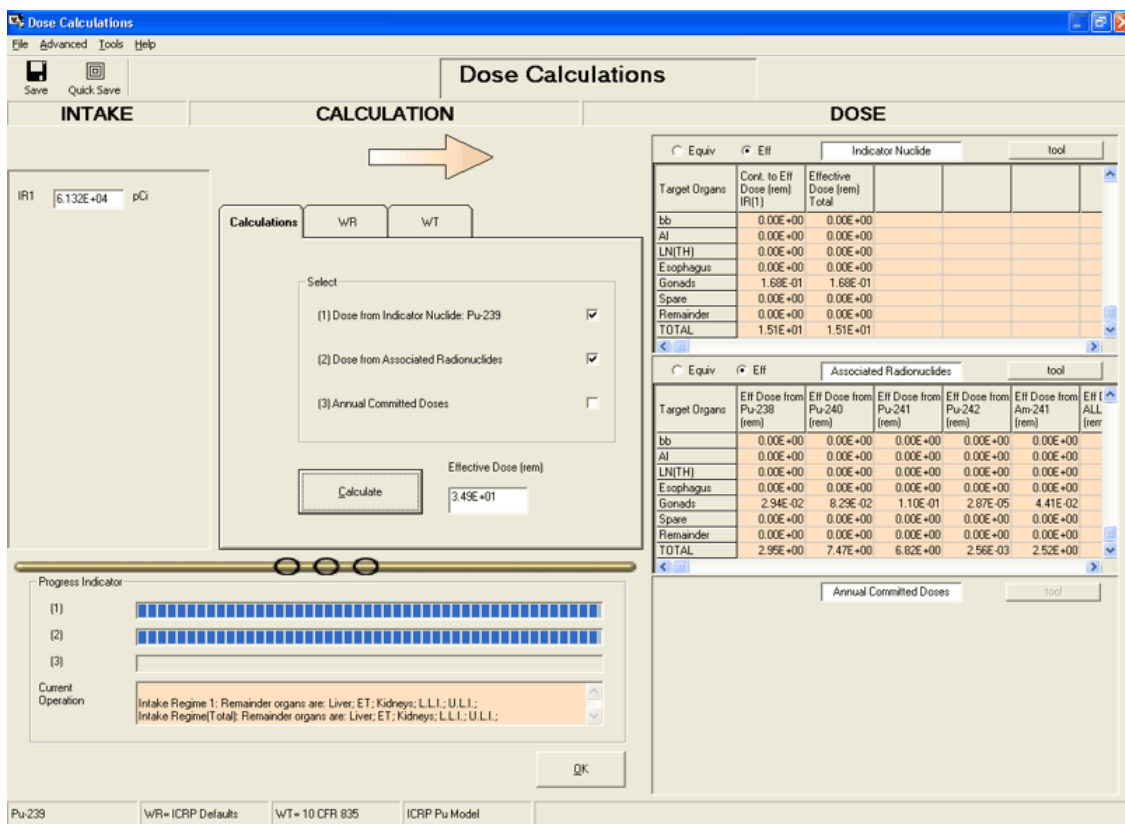


Figure D.124. Effective doses calculated using ^{239}Pu as the Indicator Nuclide.

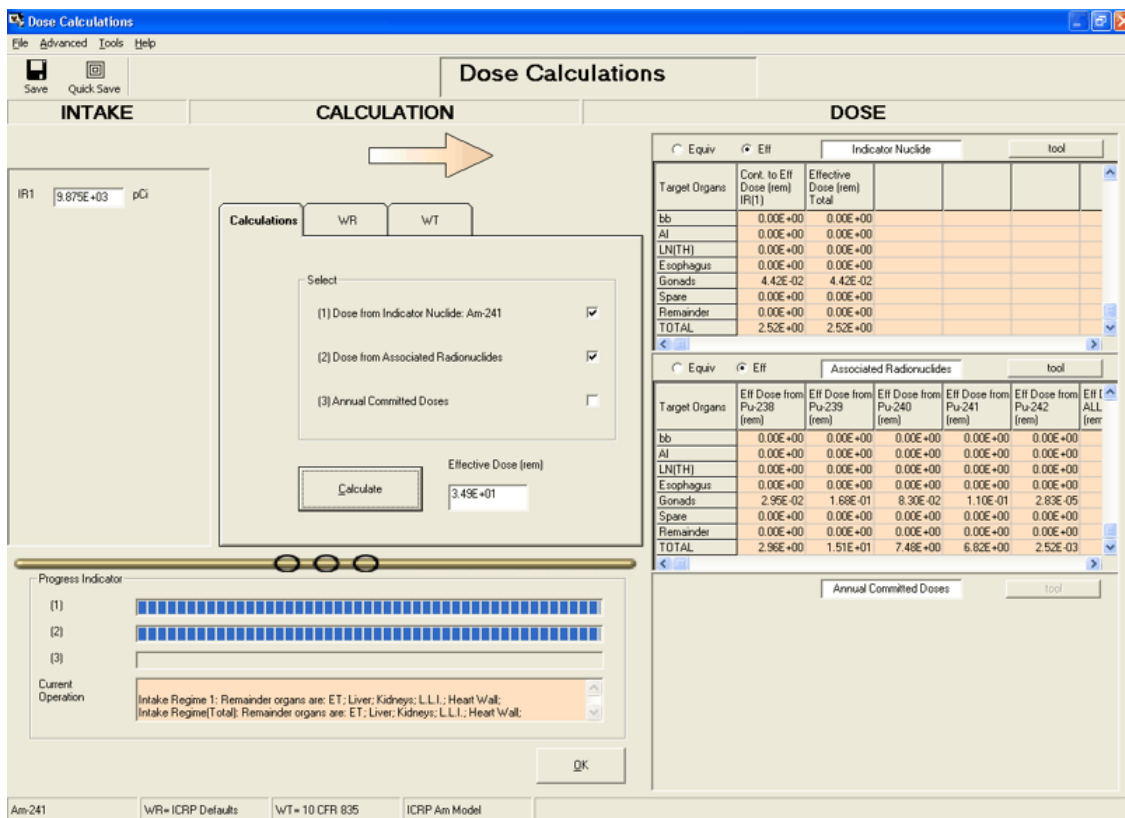
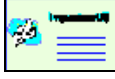


Figure D.125. Effective doses calculated using ^{241}Am as the Indicator Nuclide.

As expected, the calculated total effective dose is the same - irrespective of whether specific radionuclides are defined as the **Indicator Nuclide** or as an **Associated Radionuclide**. Table D.18 summarizes the contributions to total effective dose made by each of the 6 radionuclides involved in this example - for both of the above calculations - and the fraction of effective dose contributed by radionuclide retention in the lungs. For comparison, the Table also shows the calculated effective dose that would result from the initial assumption of Type 'S' plutonium - and all ICRP default parameter values.

Table D.18. Contributions to effective dose (in rem and %).

Contribution from:	Optimized Parameter Values - with ^{239}Pu as the Indicator Nuclide	Optimized Parameter Values - with ^{241}Am as the Indicator Nuclide	ICRP Default Parameter Values – Type 'S' Plutonium
^{238}Pu	2.95	2.96	3.05
^{239}Pu	15.1	15.1	14.9
^{240}Pu	7.47	7.48	7.30
^{241}Pu	6.82	6.82	3.93
^{242}Pu	0.00256	0.00252	0.00247
^{241}Am	2.52	2.52	2.44
Total from All Nuclides	34.9 (100%)	34.9 (100%)	31.5 (100%)
Total from Lungs	27.7 (79%)	27.7 (79%)	10.9 (39%)

	Note #1: You will have noticed that the quantity "effective dose" is remarkably "robust" (at least, for highly insoluble plutonium). In this case, the changes that we had to make to the HRTM "input" parameter values - in order to "fit" the bioassay data - changed the total effective dose only <i>marginally</i> from that calculated using standard ICRP default parameter values. Using "case specific" parameter values <i>increased</i> the calculated effective dose by just 11% !
	Note #2: However, use of "case specific" HRTM parameter values DOES have a substantial effect on the distribution of effective dose between the Lungs and other body organs . The lung dose is calculated to <i>increase</i> by a factor of about 2.5 (154%) .

D.8. Using Least Squares Fitting

To illustrate the use of the *least squares* fitting method, we will re-analyze the first example case (IAEA 1999) - which is stored in the parameter file "[Install Drv]:\\JABASOFT\\IMBAEXUS\\UserData1\\Demo\\IAEA Case 3 - 60Co.ix". This case involved an accidental inhalation of a cobalt metal and/or oxide aerosol - with whole body measurements of ^{60}Co starting at 1 d after the intake. The data were given in Table D.1.

	Note: The <i>least squares</i> fitting method can be used <i>only</i> in cases involving a <i>single intake</i> - with REAL (explicit) error values on each data point, and a <i>single bioassay quantity</i> .
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To use the *least squares* fitting method, you select this option in the **Bioassay Calculations** screen (Figures D.126 and D.127) - and click "OK".

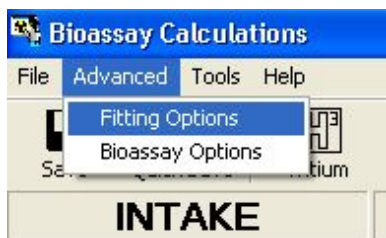


Figure D.126. Opening the "Fitting Options" menu.

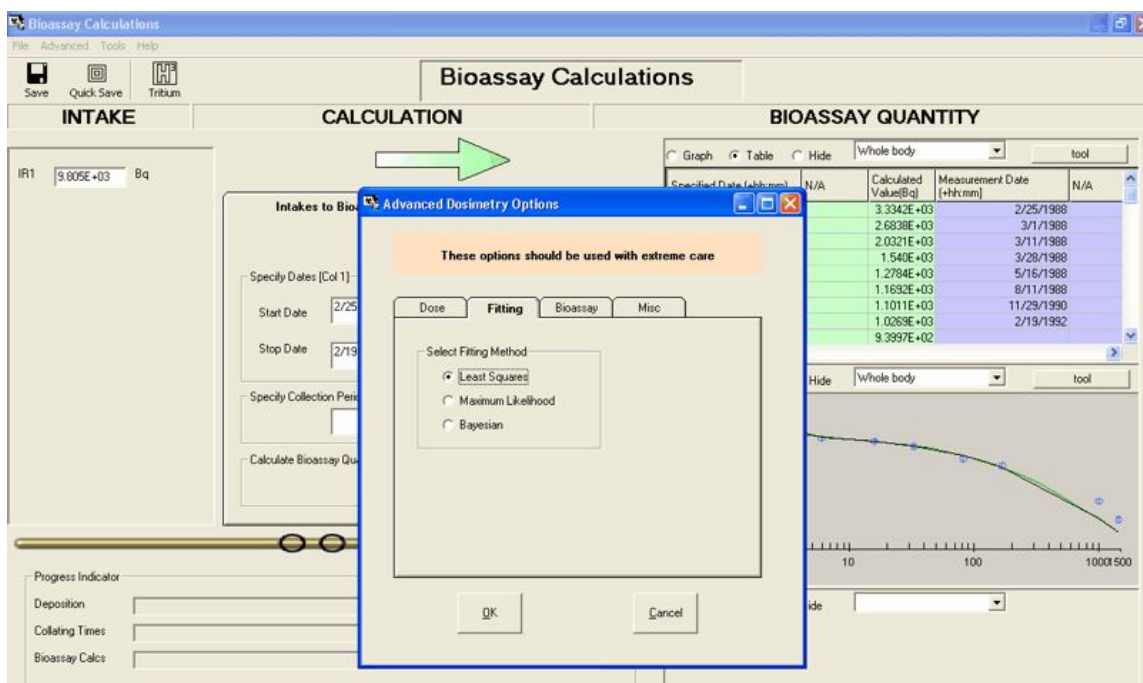


Figure D.127. Selecting the "Least Squares" Fitting option.

Back in the **Bioassay Calculations** screen, you then click the *Blue* arrow - to re-calculate the amount of **Intake (IR1)** from the tabulated bioassay data. The result is shown in Figure D.128.

As expected, the calculated value of **IR1** is **9,805 Bq** – the same value as calculated by the *maximum likelihood* method. However, the *least squares* method also calculates the *standard error* on this estimated intake - in this case **± 978.2 Bq**.



Note: More precisely, the calculated values of intake differ in the fifth significant figure - **9,805.1 Bq** for the *least squares* method c.f. **9,804.8 Bq** for the *maximum likelihood* method. This (computational) difference is *trivial*.

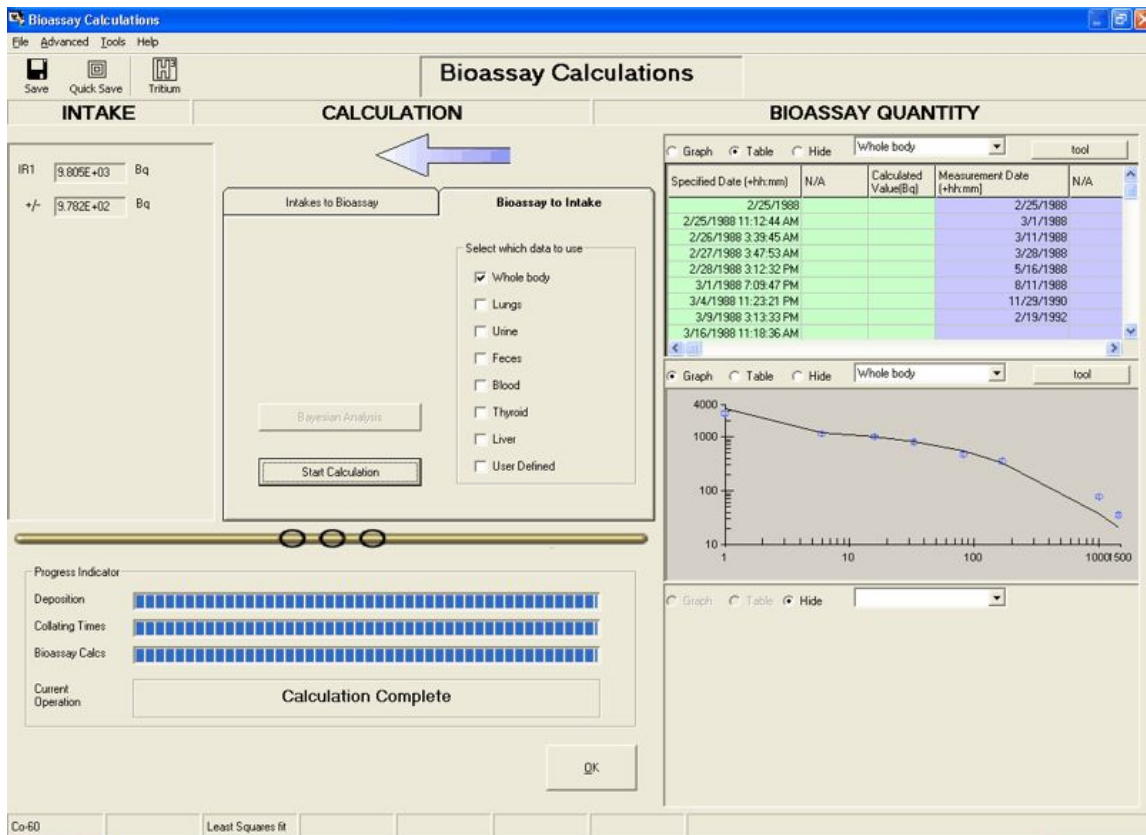


Figure D.128. Result of least squares fitting for "IAEA Case 3 - 60Co".

To further illustrate the application of the *least squares* fitting method, we can use the to "fit" the ^{241}Am chest-counting data from the HAN-1 case. Figure D.129 shows the result - for the "optimized" set of HRTM model parameters. The *least squares* method calculates an intake of **9,875 pCi (± 114.2 pCi standard error)** - c.f., the same value (**9,875 pCi**) obtained with **maximum likelihood fitting** (see Section D.7.4. entitled "Improved Representation of the HAN-1 Data").

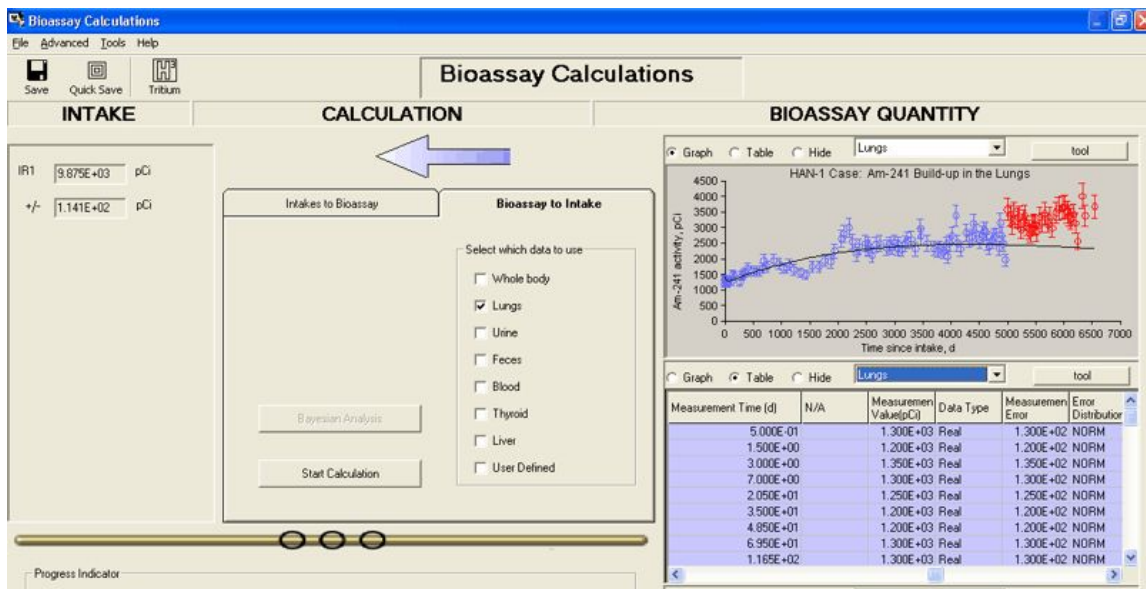


Figure D.129. Least squares "fit" of the bioassay data in the HAN-1 case.

It is also of interest to re-analyze the **HAN-1** case using the *least squares* method - with the (inappropriate) assumption of all ICRP Default HRTM parameter values and Type 'S' absorption behavior (Figure D.130).

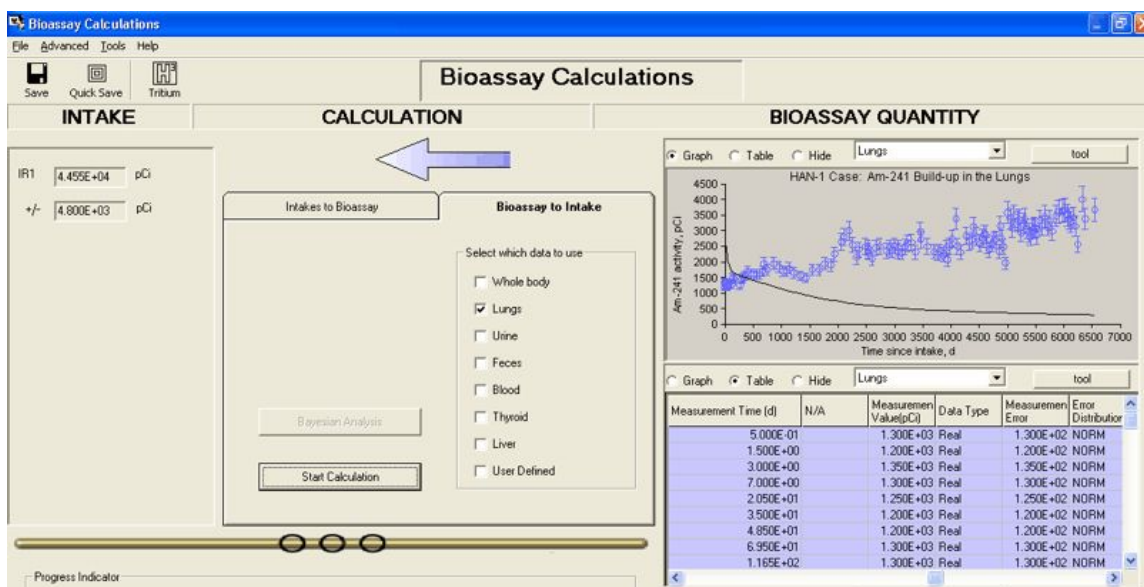


Figure D.130. Using the *least squares* method to analyze the **HAN-1** case with **ICRP default parameter values**.

Again, the *least squares* method calculates the same (to the fourth significant figure) value for the intake amount (**44,550 pCi**) as the **maximum likelihood method** - with a calculated standard error of $\pm 4,800 \text{ pCi}$ - c.f., **44,560 pCi**.

Cautionary Note: The *standard error* calculated by the *least squares* method is a *numerical statistic* only. It DOES NOT measure the "goodness of fit" of the *underlying model assumptions*. Hence, the *relative standard error* is the same for the "fits" shown in Figures D.129 and D.130 - whereas, in Figure D.130, the "model" clearly DOES NOT "fit" the data! The overall "goodness of fit" of the model is measured by the χ^2 -sum statistic.

D.9. Using Bayesian Analysis

To illustrate the use of the *Bayesian inference* in the fitting procedure, we will again re-analyze the first example case (IAEA 1999) - stored in the parameter file "[Install Drv]:\JABASOFT\IMBAEXUS\UserData1\Demo\IAEA Case 3 - 60Co - Bayes.ix". This case involved an accidental inhalation of a cobalt metal and/or oxide aerosol - with whole body measurements of ^{60}Co starting at 1 d after the intake. The data were given in Table D.1.

Note: In **IMBA Expert™ OCAS/ORAU-Edition - Version 3.2.04**, extension of *Bayesian Analysis* to *multiple intakes* has not yet been fully implemented. This is still under development. It will be provided as an automatic "update" to Version 3.2.

An introduction to Bayesian inference, and a description of how this is implemented in [IMBA Expert™ OCAS/ORAU-Edition](#), is given in the section of **Appendix A: Technical Basis** entitled "Using Bayesian Inference". That description includes the types of Bayesian Prior probability distribution that are available in this version of the software.

To use the "**Bayesian**" **Fitting** option, you must first *select* this - from the **Bioassay Calculation** screen's **Advanced | Fitting Options** menu (Figure D.131).

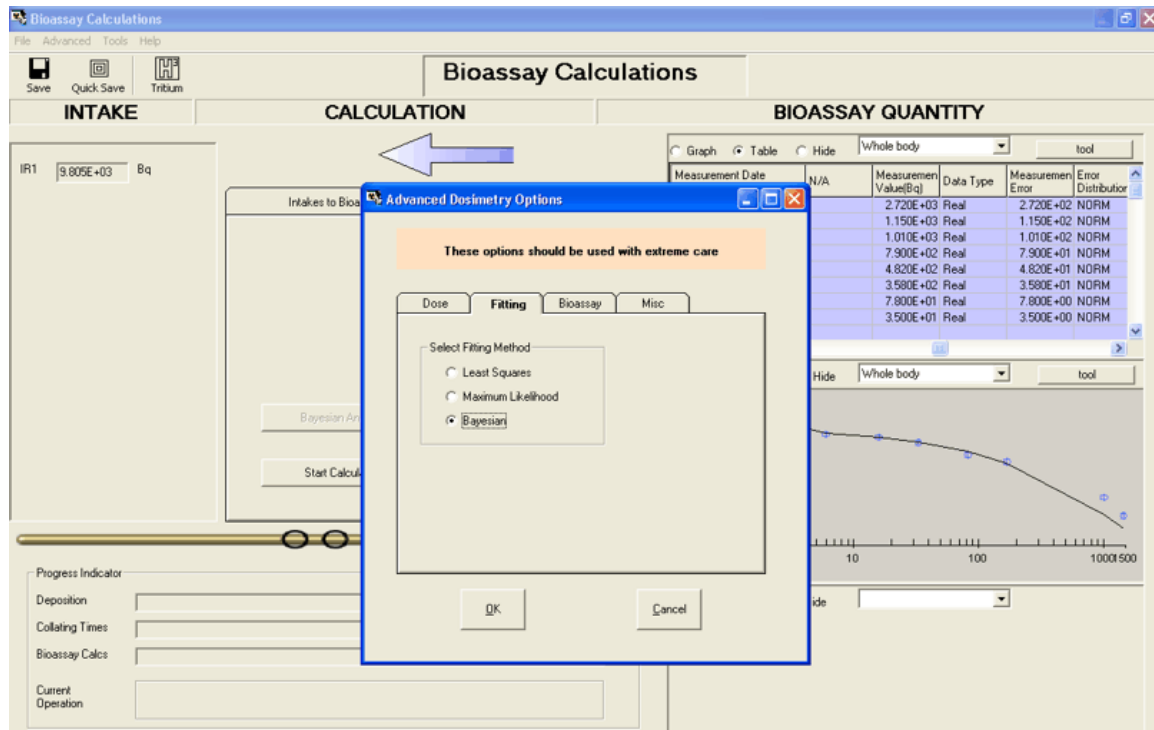


Figure D.131. Selecting the "**Bayesian**" **Fitting** option.

This will *activate* the "**Bayesian Analysis**" button in the **Bioassay Calculations** screen (Figure D.132).

Clicking the "**Bayesian Analysis**" button opens a new screen - the **Bayesian Analysis** tool (Figure D.133).



Tip: Figure D.131 shows the "**default**" settings of the **Bayesian Analysis** tool – for the type of prior (*defaulted* to "**Uniform**"), the X- and Y- axis ranges, and for display of the "**Log Likelihood Function**". Other types of *prior* are *selected* using radio buttons (bottom-left-corner). The other types of function ("**Prior Distribution**" or "**Probability of Intake**") are also *selected* using radio buttons (top-right-corner).

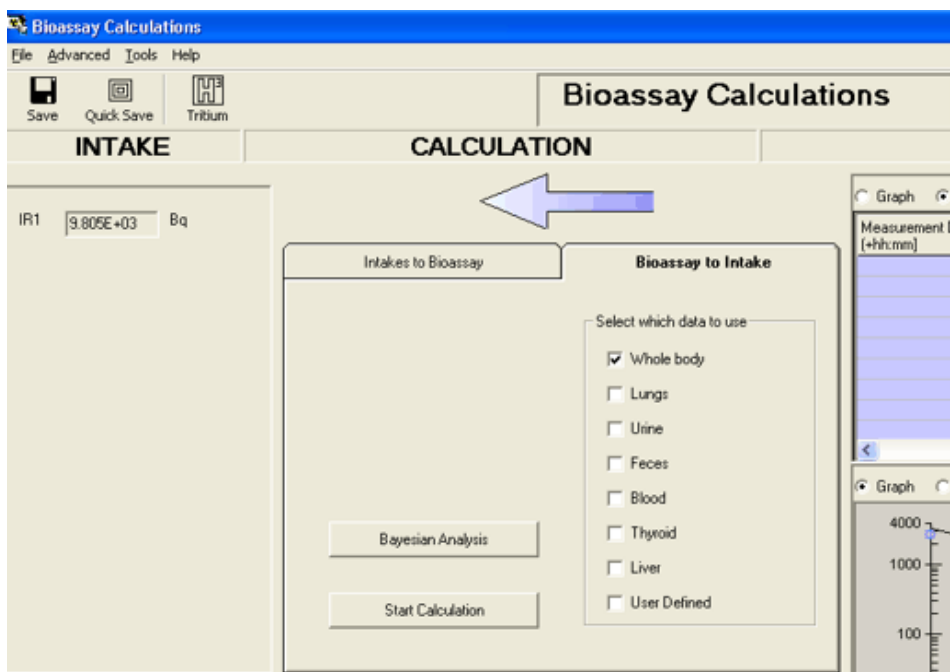


Figure D.132. "Bayesian Analysis" button activated.

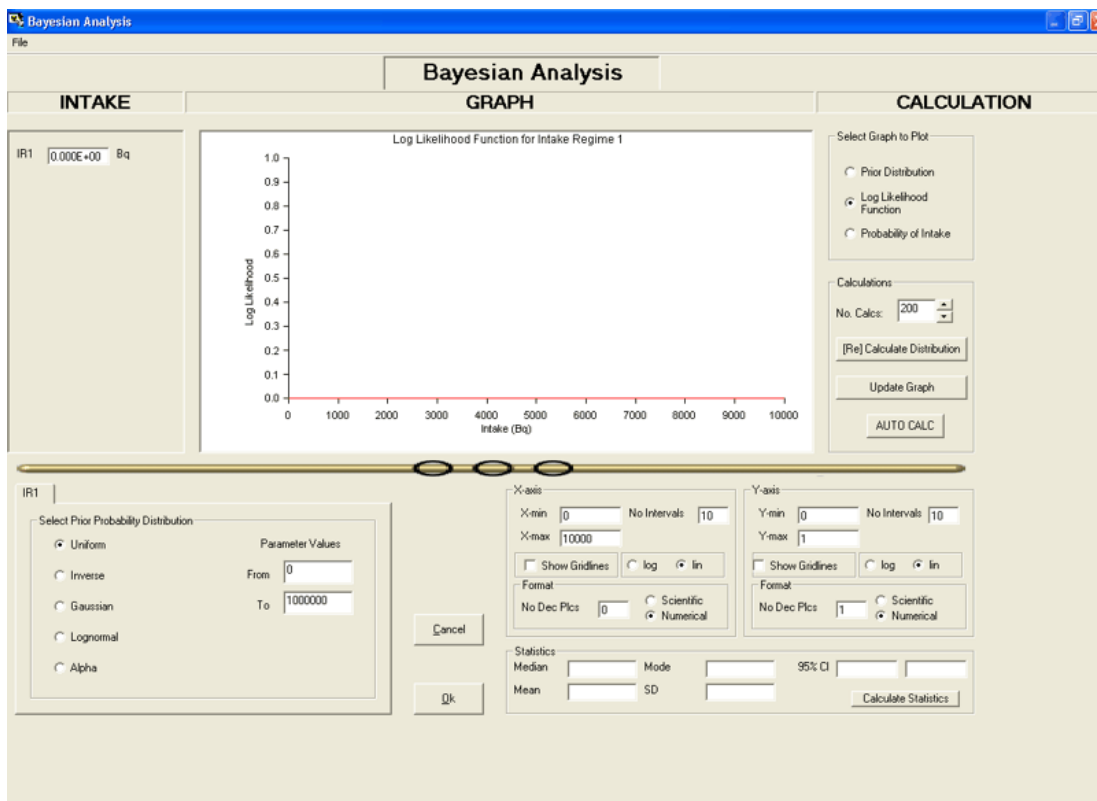


Figure D.133. Bayesian Analysis screen as it appears for a "New" case - with no bioassay data loaded.

If you have previously calculated the amount of intake (e.g., using the *maximum likelihood* or *least squares* method), the **X-axis** in the **Bayesian Analysis** tool will "auto-range" accordingly - when the tool is opened (Figure D.134).

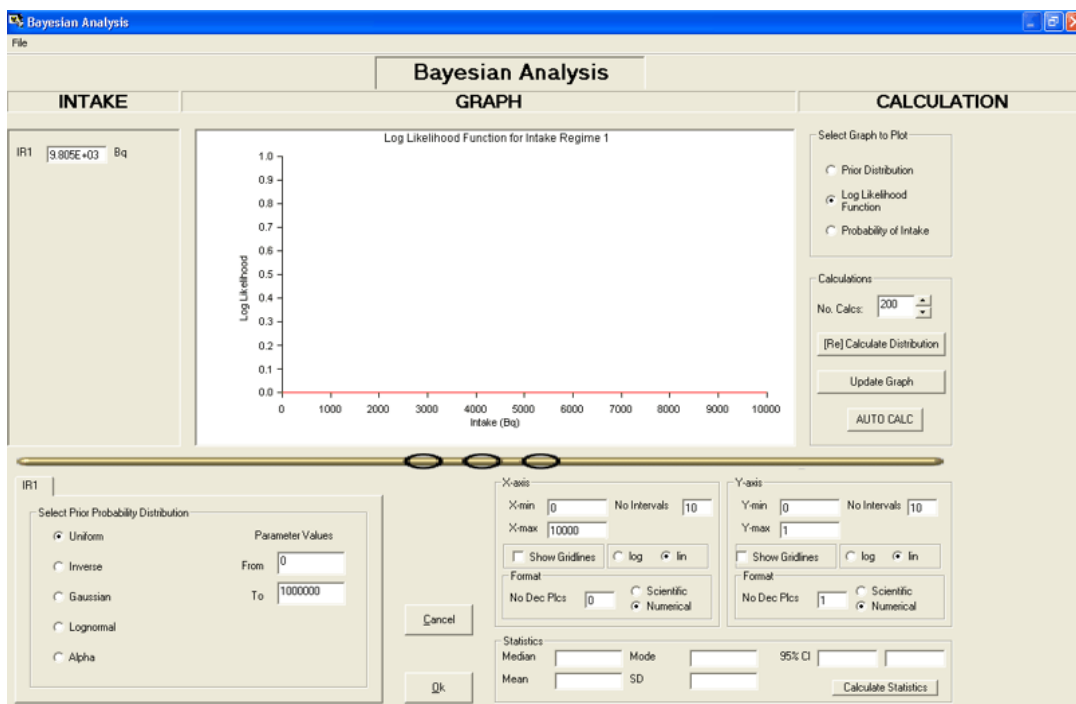


Figure D.134. "Auto-ranging" of X-axis when the intake amount (**IR1**) has already been calculated.

Note: The Y-axes also "auto-ranges" when you calculate the other types of probability distribution. However, the X-axis DOES NOT. You have to *choose* the appropriate X-axis range - to include the whole calculated distribution.

In the next sections, we will show how each type of "**Prior Distribution**" affects the calculated "**Log Likelihood Function**" and the posterior probability distribution of intake ("**Probability of Intake**") in the "IAEA Case 3" ⁶⁰Co whole body monitoring example - as follows:

- Uniform prior.
- Inverse prior.
- Gaussian prior.
- Lognormal prior.
- 'Alpha' prior.

D.9.1. Probability Distribution of Intake Assuming a Uniform Prior

Figure D.135 shows the starting point for **Bayesian Analysis** of the bioassay data in "IAEA Case 3" - the calculation (and display) of the "**Prior Distribution**". In this case, we have selected "**Uniform**" as the "**Prior Probability Distribution**" type - and clicked the "**AUTO CALC**" button (middle-right-side of the **Bayesian Analysis** tool).

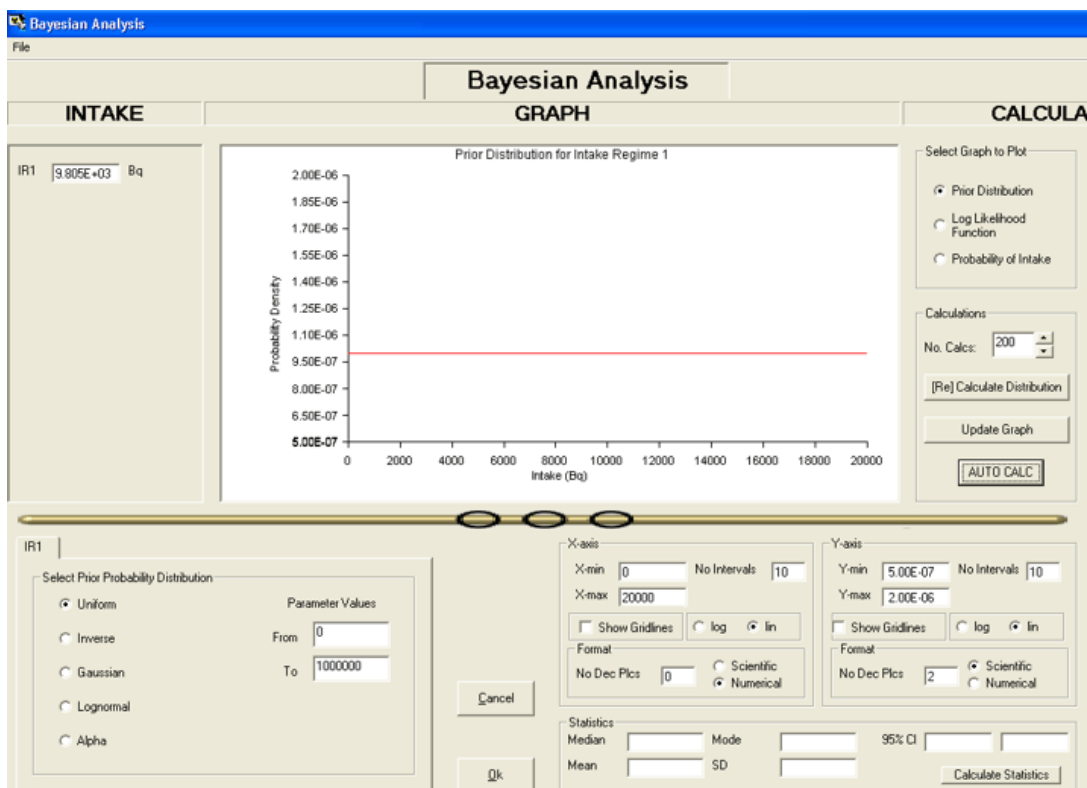


Figure D.135. "Prior Distribution" calculated (and displayed) over a suitable X-axis range.

Cautionary Note: Before you can use the **Bayesian Analysis** tool to calculate (and display) the posterior probability distribution of intake, you must **FIRST** calculate (for your selected prior distribution) the *median* value of the intake distribution. You do this back in the **Bioassay Calculations** screen - by clicking the "**Start Calculations**" button (just as you do for *maximum likelihood* or *least squares* fitting).

To calculate (and display) the Log Likelihood Function, you simply *click* its radio button - and *click* "**AUTO CALC**" again. The calculated **Log Likelihood Function** is shown in Figure D.136.

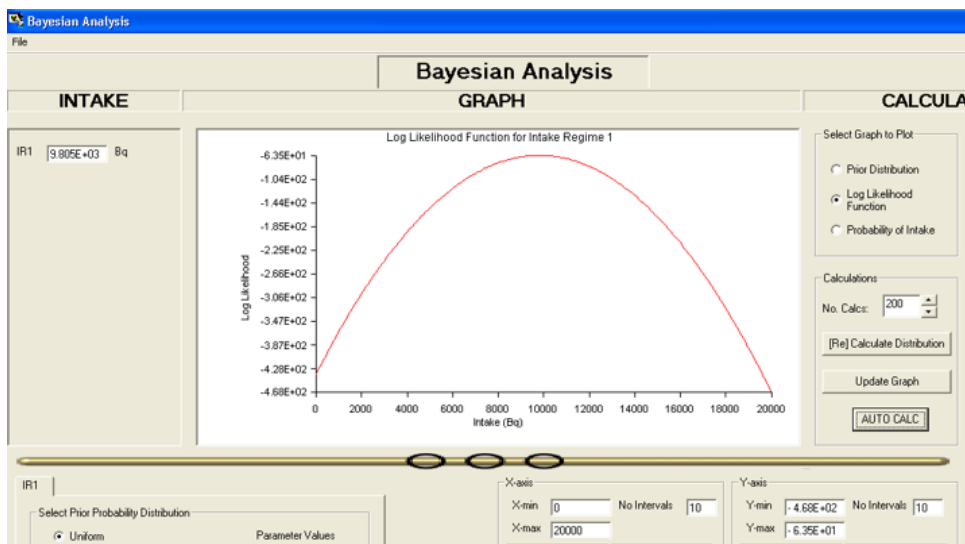


Figure D.136. Calculated Log Likelihood Function.



Tip: Notice here that the Y-axis has "auto-ranged" - but the X-axis range has retained its initial setting.



Note: The Log Likelihood Function, $P(m|I)$, is independent of the *prior*. It is the logarithm of the **Likelihood Function**, *i.e.*, the logarithm of the likelihood of observing ALL of the measured values (*m*) expressed as a function of intake (*I*). This depends only on the measurements and the bioassay function.

To calculate the posterior probability distribution, *i.e.*, the "**Probability of Intake**", you simply *click* its radio button - and then *click* "**AUTO CALC**" again. The result is shown in Figure D.137.

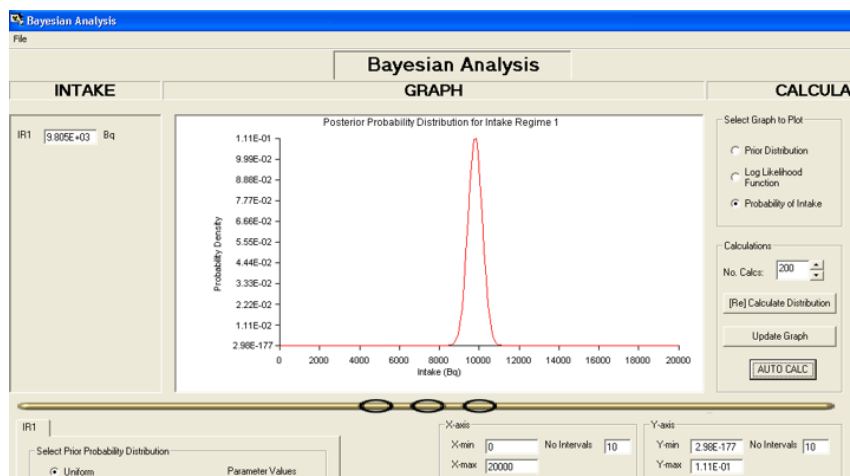


Figure D.137. Calculated **Probability of Intake** - for a *uniform* prior.

To calculate the statistical parameters of this distribution, you simply click the "**Calculate Statistics**" button (bottom-right-corner of the **Bayesian Analysis** tool). The results are automatically displayed (Figure D.138).

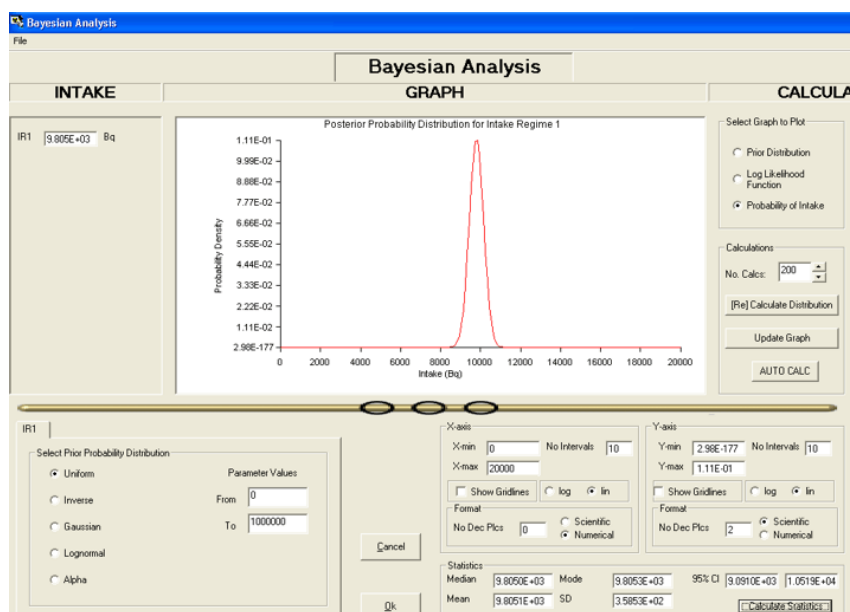


Figure D.138. Calculating and displaying the **statistical parameters** of the posterior probability distribution of intake.

In this example, the statistical parameters of the intake distribution are:

- **Median:** 9,805.0 Bq.
- **Mean:** 9,805.1 Bq.
- **Mode:** 9,805.3 Bq.
- **Standard Deviation:** 358.53 Bq.
- **95% Confidence Interval:** 9,091 - 10,519 Bq.

	Note #1: This distribution is very close to <i>normal</i> (symmetrical).
	Note #2: As expected, the calculated <i>median</i> of the posterior probability distribution of intake (9,805 Bq) is IDENTICAL to the mean value calculated by least squares - but the <i>standard deviation</i> of the intake distribution (358.5 Bq) is NOT the same as the <i>standard error</i> of the intake calculated by least squares (978.2 Bq).

D.9.2. Probability Distribution of Intake Assuming an Inverse Prior

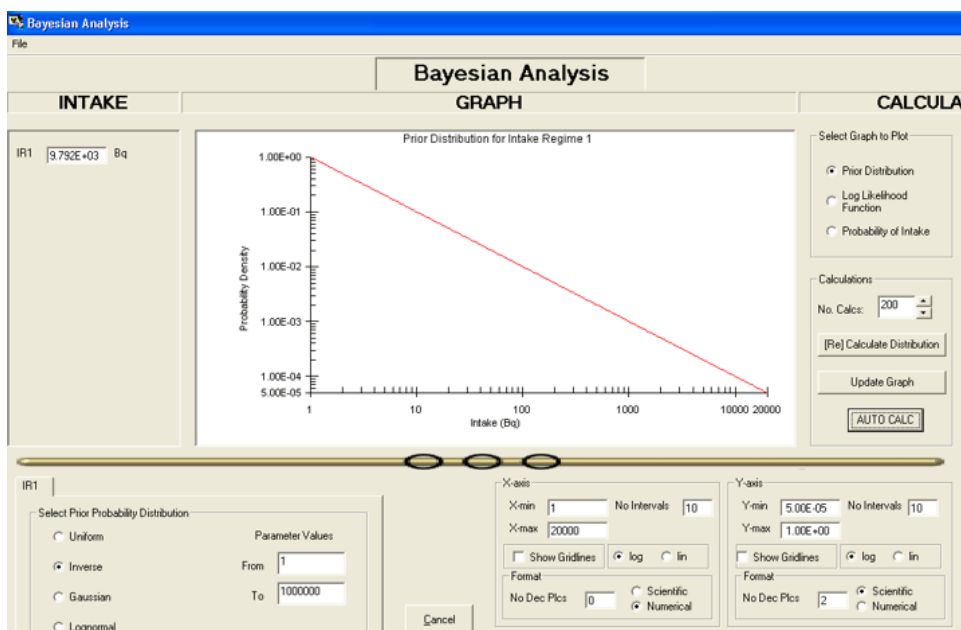


Figure D.139. Inverse prior - plotted on Log-Log axes.

The Inverse prior probability distribution is shown in Figure D.139. With this prior, the calculated *median* value of the intake distribution is **9,793 Bq** (c.f., **9,805 Bq** for the *uniform* prior). The calculated **Log Likelihood Function** (which is independent of the prior) was shown in Figure D.136 (for the *uniform* prior).

The calculated posterior probability distribution of intake is shown in Figure D.140, together with the calculated statistical parameters of this distribution.

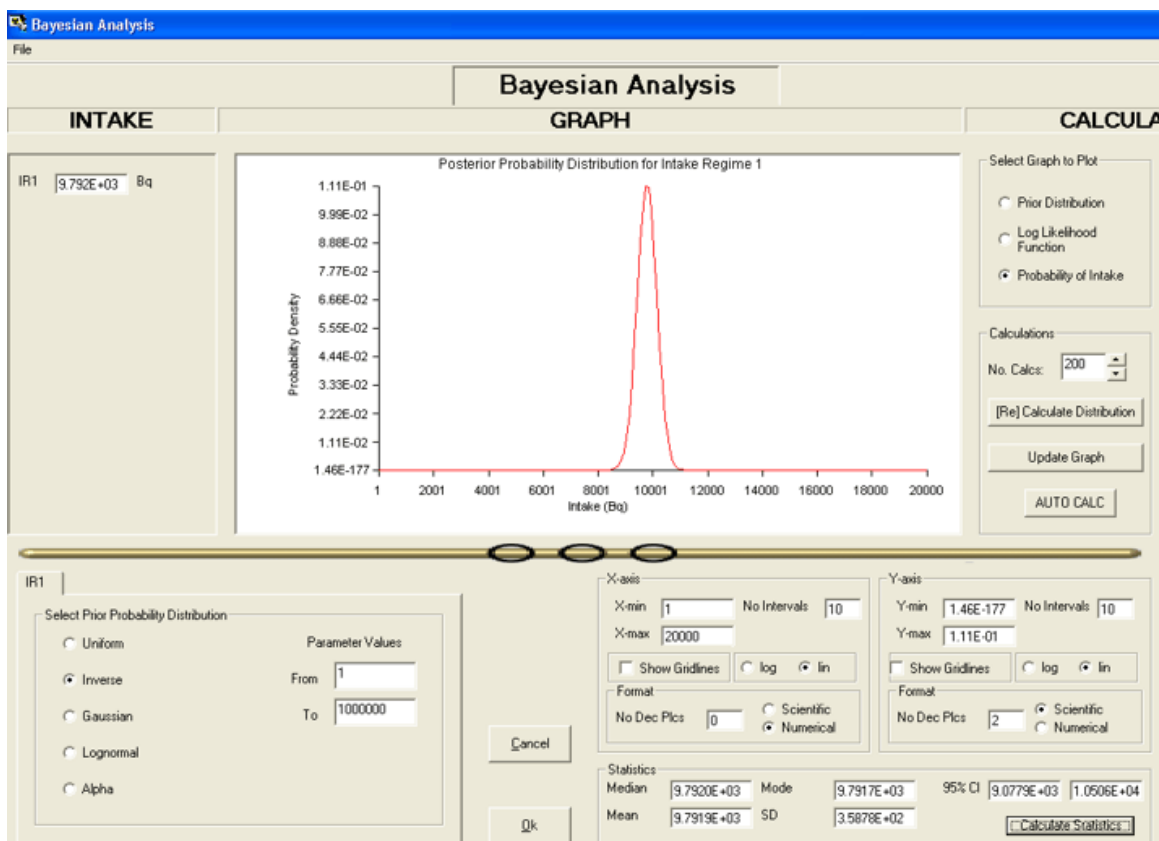


Figure D.140. Posterior probability distribution of intake calculated for the *inverse* prior.

In this example, the statistical parameters of the intake distribution are:

- **Median:** 9,792.0 Bq.
- **Mean:** 9,791.9 Bq.
- **Mode:** 9,791.7 Bq.
- **Standard Deviation:** 358.78 Bq.
- **95% Confidence Interval:** 9,078 - 10,506 Bq.

Note: This posterior distribution is very close to *normal* (symmetrical) - as was the case for the *uniform* prior. However, the distribution has been *shifted* (very slightly) to *lower* values of the median, mean and mode.

D.9.3. Probability Distribution of Intake Assuming a Gaussian Prior

A Gaussian prior probability distribution is shown in Figure D.141. The *median* (= *mean*) of this distribution is 2,000 Bq, and the standard deviation 1,500 Bq. With this prior, the calculated *median* value of the intake distribution is **9,383 Bq** (c.f., **9,805 Bq** for the *uniform* prior). The calculated **Log Likelihood Function** (which is independent of the prior) was shown in Figure D.136 (for the *uniform* prior).

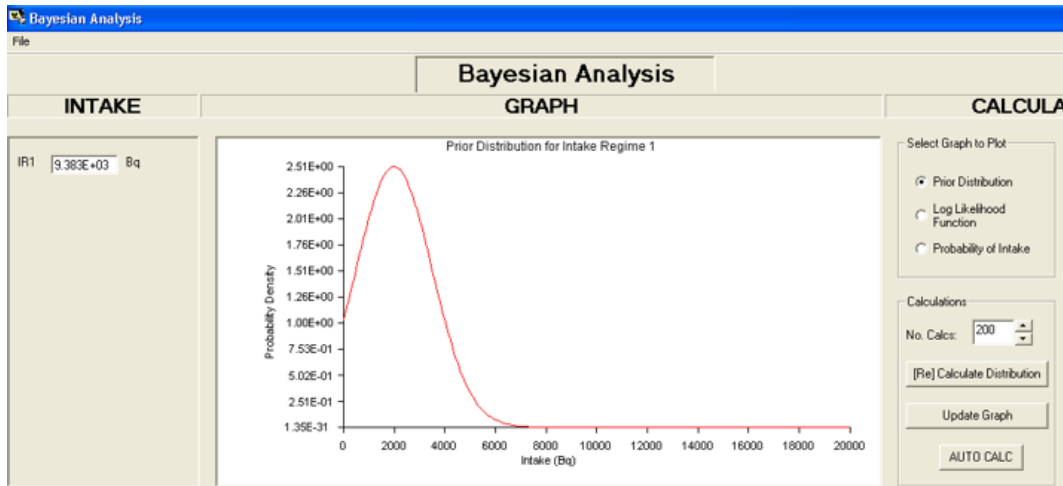


Figure D.141. Example of a **Gaussian** prior.

The calculated posterior probability distribution of intake is shown in Figure D.142, together with the calculated statistical parameters of this distribution.

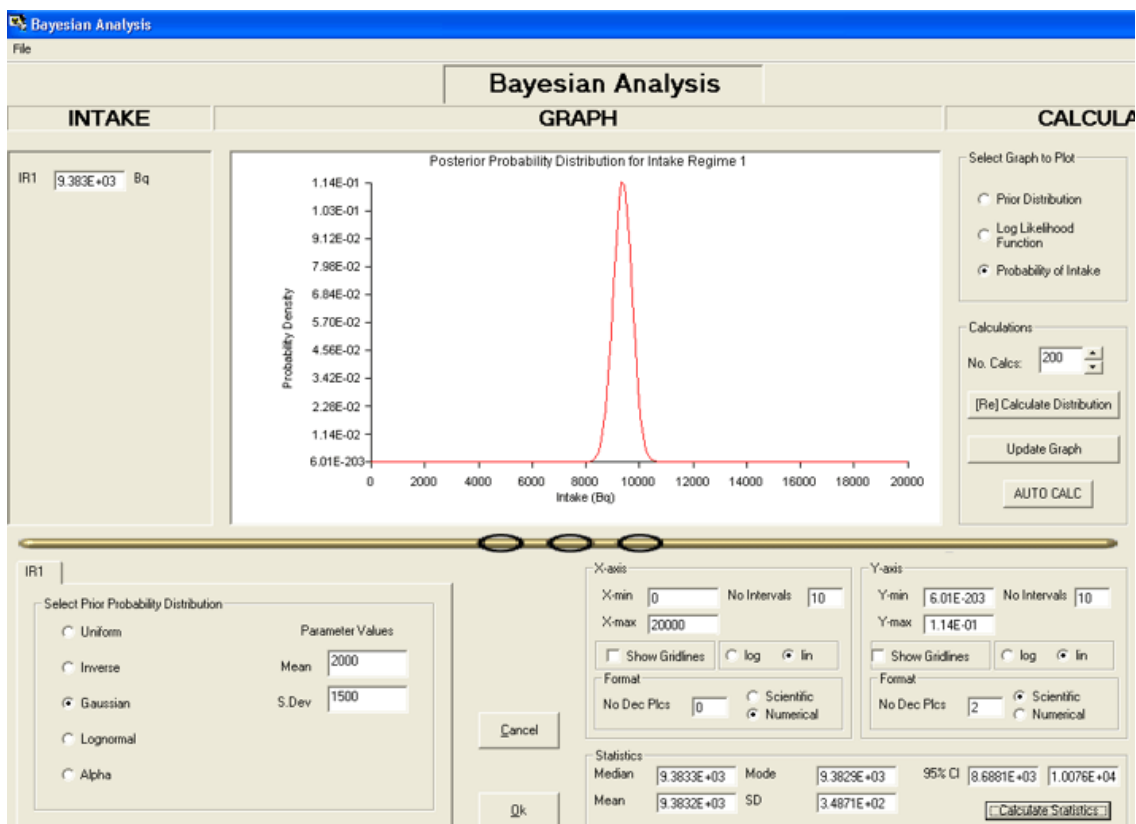


Figure D.142. Posterior probability distribution of intake calculated for a *Gaussian* prior.

In this example, the statistical parameters of the intake distribution are:

- **Median:** 9,383.3 Bq.

- **Mean:** 9,383.2 Bq.
- **Mode:** 9,382.9 Bq.
- **Standard Deviation:** 348.71 Bq.
- **95% Confidence Interval:** 8,688 - 10,076 Bq.



Note: Again, this posterior distribution is very close to *normal* (symmetrical) - as was the case for the *uniform* prior. However, in this example, the distribution has been *shifted* to *lower* values of the median, mean and mode. The amount of "shift" depends on BOTH the assumed *median* (= *mean*) value AND the *standard deviation* of the *Gaussian* prior.

D.9.4. Probability Distribution of Intake Assuming a Lognormal Prior

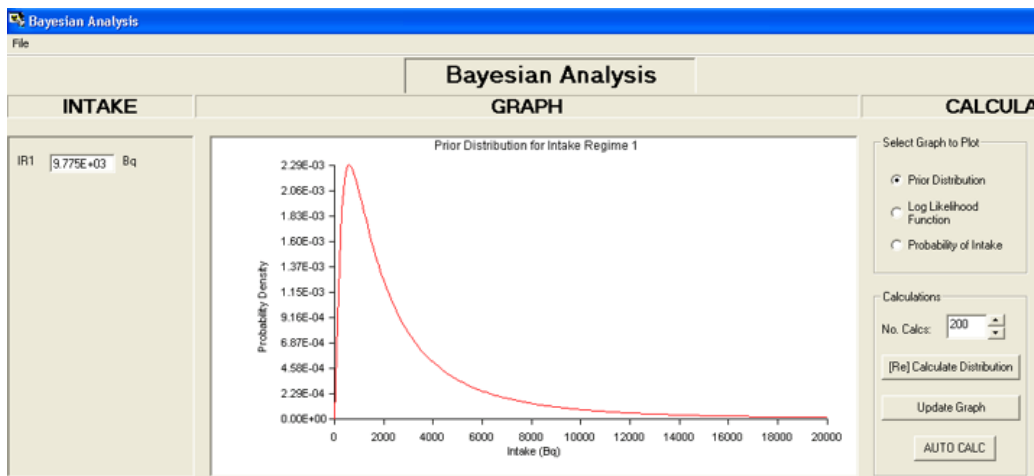


Figure D.143. Example of a **Lognormal** prior.

A Lognormal prior probability distribution is shown in Figure D.143. The *median* ($\neq$ *mean*) of this distribution is 2,000 Bq, and the geometric standard deviation is 3. With this prior, the calculated *median* value of the intake distribution is **9,775 Bq** (c.f., **9,805 Bq** for the *uniform* prior). The calculated **Log Likelihood Function** (which is independent of the prior) was shown in Figure D.136 (for the *uniform* prior).

The calculated posterior probability distribution of intake is shown in Figure D.144, together with the calculated statistical parameters of this distribution.

In this example, the statistical parameters of the intake distribution are:

- **Median:** 9,774.7 Bq.
- **Mean:** 9,774.6 Bq.
- **Mode:** 9,774.3 Bq.
- **Standard Deviation:** 358.89 Bq.
- **95% Confidence Interval:** 9,062 - 10,489 Bq.

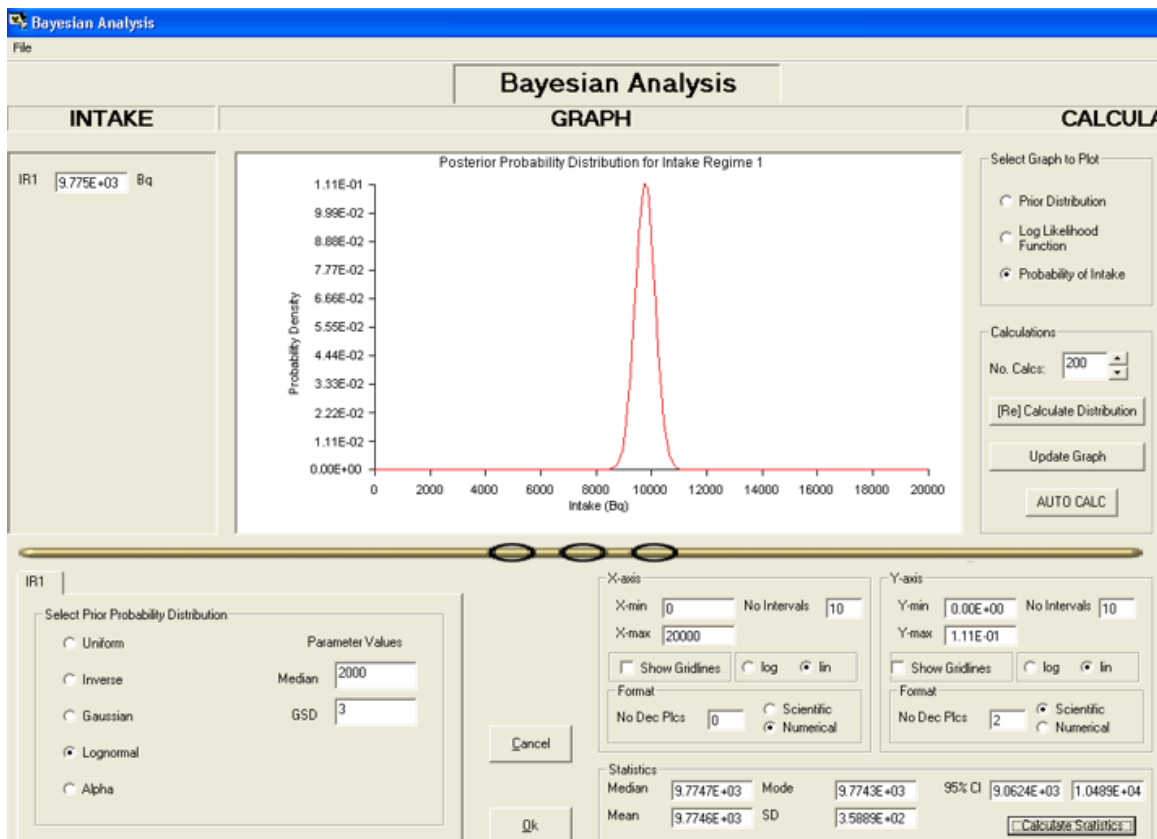


Figure D.144. Posterior probability distribution of intake calculated for a *Lognormal* prior.

Note: Again, this posterior distribution is very close to *normal* (symmetrical) - as was the case for the *uniform* prior. However, in this example, the distribution has been *shifted* to *marginally lower* values of the median, mean and mode. The amount of "shift" depends on BOTH the assumed *median* ($\neq$ *mean*) value AND the geometric *standard deviation* of the *Lognormal* prior.

D.9.5. Probability Distribution of Intake Assuming an 'Alpha' Prior

An 'Alpha' prior probability distribution is shown in Figure D.145. This example is defined by an '**Alpha**' value of **0.001**, and an '**Imax**' value of **100,000**. The calculated *median* of this distribution is **50.79 Bq**, with a very large *standard deviation* of **4,737.2 Bq**. With this prior, the calculated *median* value of the intake distribution is **9,805 Bq** - which is identical to the value for the *uniform* prior. The calculated **Log Likelihood Function** (which is independent of the prior) was shown in Figure D.136 (for the *uniform* prior).

The calculated posterior probability distribution of intake is shown in Figure D.146, together with the calculated statistical parameters of this distribution.

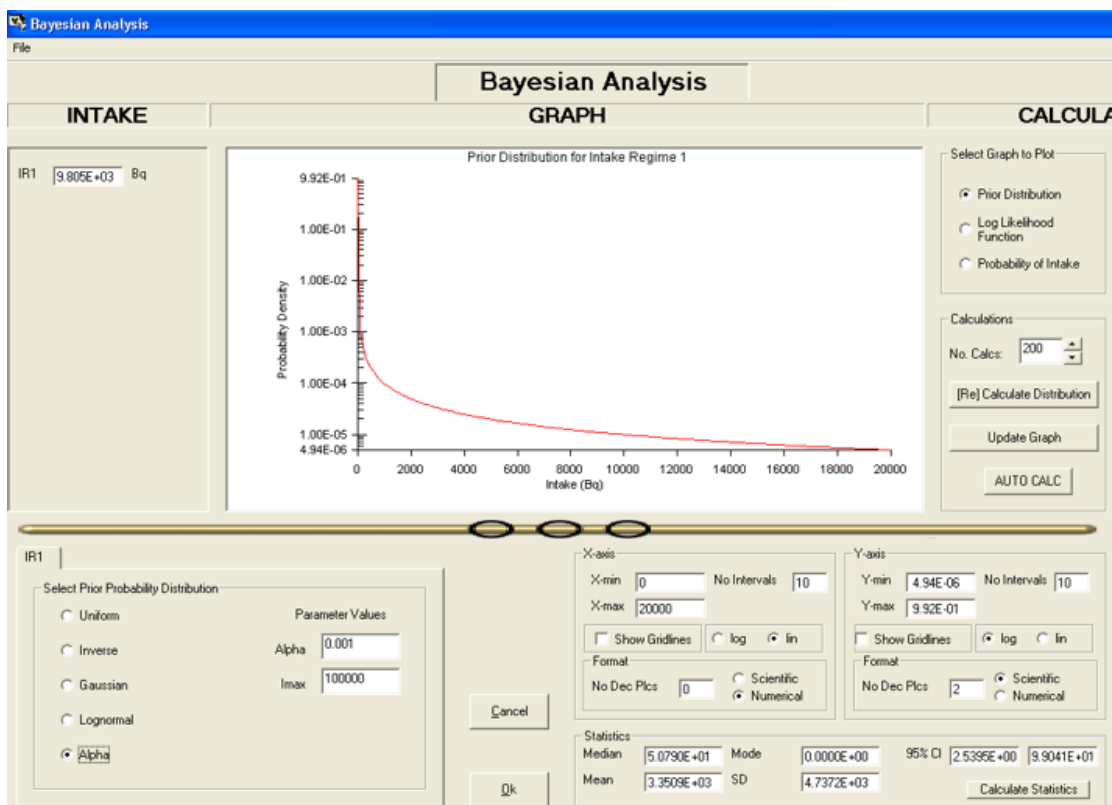


Figure D.145. Example of an 'Alpha' prior.

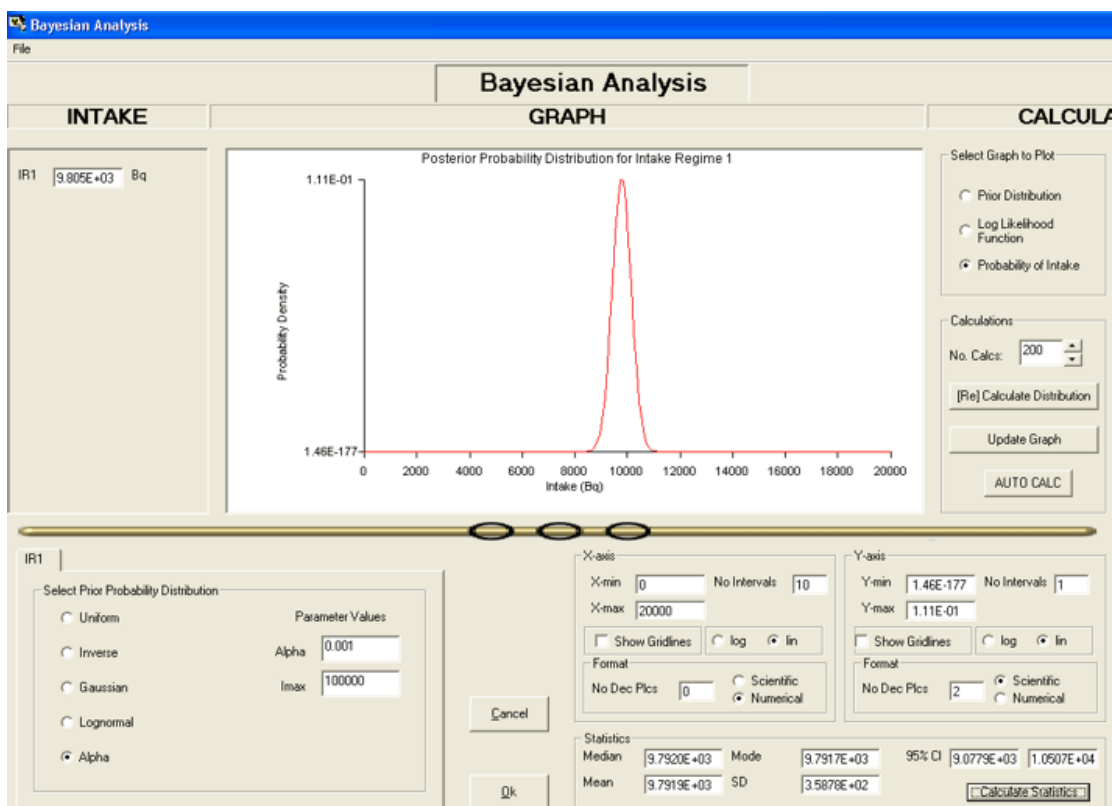


Figure D.146. Posterior probability distribution of intake calculated for an 'Alpha' prior.

In this example, the statistical parameters of the intake distribution are:

- **Median:** 9,792.0 Bq.
- **Mean:** 9,791.9 Bq.
- **Mode:** 9,791.7 Bq.
- **Standard Deviation:** 358.78 Bq.
- **95% Confidence Interval:** 9,078 - 10,507 Bq.



Note: Again, this posterior distribution is very close to *normal* (symmetrical) - as was the case for the *uniform* prior. However, in this example, the distribution has been shifted to marginally lower values of the median, mean and mode.

D.10. Transdermal Uptake of ^{125}I from a Wound

In this case, a laboratory worker received an accidental needle-puncture wound (on the thumb) while performing iodinations. The total amount of ^{125}I used in the procedure was about 2 mCi, but only a small fraction of this was still in the syringe at the time of the incident. A thyroid measurement was made within a few hours, and followed up with 4 further measurements over the next 34-d period. 'Background' thyroid measurements were available both prior to the incident, and at 75 and 138 d afterwards. After washing the wound, the estimated (retained) activity was about 300 nCi. At 4 d after the incident, the ^{125}I activity at the wound site had fallen to about 3.5% of the original measurement. At 7 d, the ^{125}I activity at the wound site remained at about 3.5% of the original measurement. At 13 d, the ^{125}I activity at the wound site had dropped to about 1.8%.

The thyroid measurements are given in Table D.19.

Table D.19. ^{125}I activity measured in the thyroid.

Approximate time relative to puncture-wound (d)	Thyroid activity $\pm$ standard error (pCi)
-177	5,000 $\pm$ 2,000
-151	2,000 $\pm$ 3,000
0.1	6,000 $\pm$ 2,000
4	14,000 $\pm$ 3,000
7	10,000 $\pm$ 3,000
13	15,000 $\pm$ 3,000
34	16,000 $\pm$ 3,000
75	3,000 $\pm$ 3,000
138	9,000 $\pm$ 2,000

Figure D.147 shows the data values as entered (from the date + time information) in the **Table Tool** of [IMBA Expert™ OCAS/ORAU-Edition](#).

Table Tool : Thyroid Data									
	Specified Time (d)	N/A	Calculated Value(pCi)	Measurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution
1				-1.769166667E+02		5.000E+03	Real	2.000E+03	NORM
2				-1.509166667E+02		2.000E+03	Real	3.000E+03	NORM
3				8.333333333E-02		6.000E+03	Real	2.000E+03	NORM
4				4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM
5				7.083333333E+00		1.0000E+04	Real	3.000E+03	NORM
6				1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM
7				3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM
8				7.508333333E+01		3.000E+03	Real	3.000E+03	NORM
9				1.380833333E+02		9.000E+03	Real	2.000E+03	NORM
10									

Figure D.147. Input data on thyroid uptake of ^{125}I with assumed error distributions.

D.10.1. Setting Up the 'Wound' Intake Scenario

The necessary steps (carried out in the **Main Screen**) are:

1. Set the **Reference Date**, i.e., the **Date** and **Time** of the incident.
2. Select the **Indicator Nuclide**, i.e., **Iodine-125**.
3. Select the **"Wound"** radio button to define the **Intake Scenario** – in the **"Model Parameters"** panel (Figure D.148).

Selecting **"Wound"** as the **Intake Scenario** will automatically activate the **"Wound"** model button (displayed in pink in Figure D.148).

The screenshot displays the IMBA Expert™ OCAS-Edition software interface. The top menu bar includes File, Edit, Parameters, Calculations, Tools, Advanced, and Help. The main window is divided into several panels. The 'Intake Scenario' panel on the left shows 'IR 1' selected, with 'Route' set to 'Wound' and 'Mode' set to 'Acute'. The 'Indicator Nuclide' panel on the right shows 'I-125' selected. The 'Model Parameters' panel at the bottom left shows 'Wound' selected under 'Respiratory Tract'. The 'Calculations' panel at the bottom right shows 'Bioassay Calculations' and 'Dose Calculations' buttons. The status bar at the bottom indicates 'Wound: Not Specified'.

Figure D.148. Main Screen with activated button to define the **"Wound"** model.

Click the **"Wound"** model button to open the **'Generic Wound Model'** window (Figure D.149).

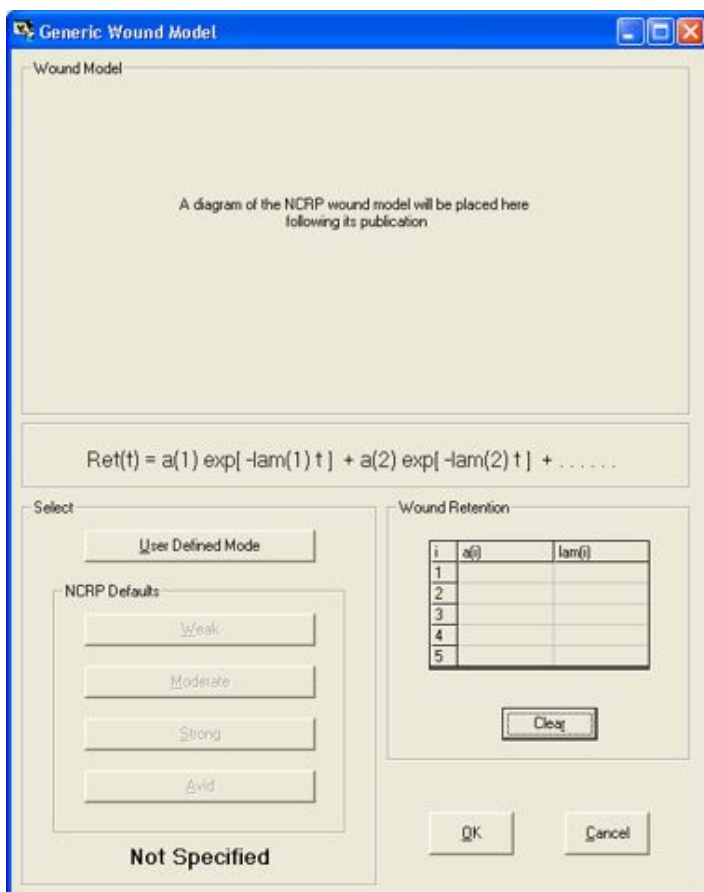


Figure D.149. The 'Generic Wound Model' window.

At this time (March, 2004), the National Council on Radiological Protection (NCRP) has not yet recommended specific parameter values to represent retention of different types of material in a sub-cutaneous "wound". Therefore, [IMBA Expert™ OCAS/ORAU-Edition](#) has incorporated a "generic" form of "wound model", in which retention is represented by the sum of a series of exponentially decaying terms (Figure D.149). You can define up to five exponential terms in the "User Defined Mode" by clicking the so-named button (Figure D.150).

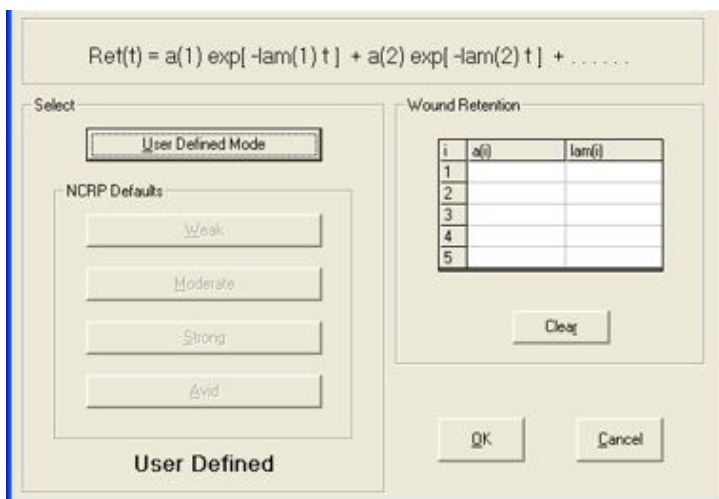


Figure D.150. User Defined Mode for entering a "Wound Retention" function.

For all compounds of iodine, ICRP Publication 68 (ICRP 1994b) recommended Type 'F' to represent absorption from the respiratory tract (at a characteristic rate of 100 d^{-1}), with a GI-tract absorption fraction of 1. Therefore, as a first "guess", it is reasonable to assume very rapid uptake of the ^{125}I "iodination" compound from the puncture-wound involved in this incident. We can represent this simply by entering the following values for the retention parameters (as shown in Figure D.151):

- $a(1) = 1$;
- $\text{lam}(1) = 100 \text{ d}^{-1}$.

i	a(i)	lam(i)
1	1	100
2		
3		
4		
5		

Figure D.151. Setting the rate constant for retention in a wound as 100 d^{-1} .

In the next section, we will test how well this assumed rapid elimination rate from the wound site "fits" the measured time-course of ^{125}I uptake and retention in the thyroid.

D.10.2. Testing the 'Default' Assumption of 'Rapid' Uptake

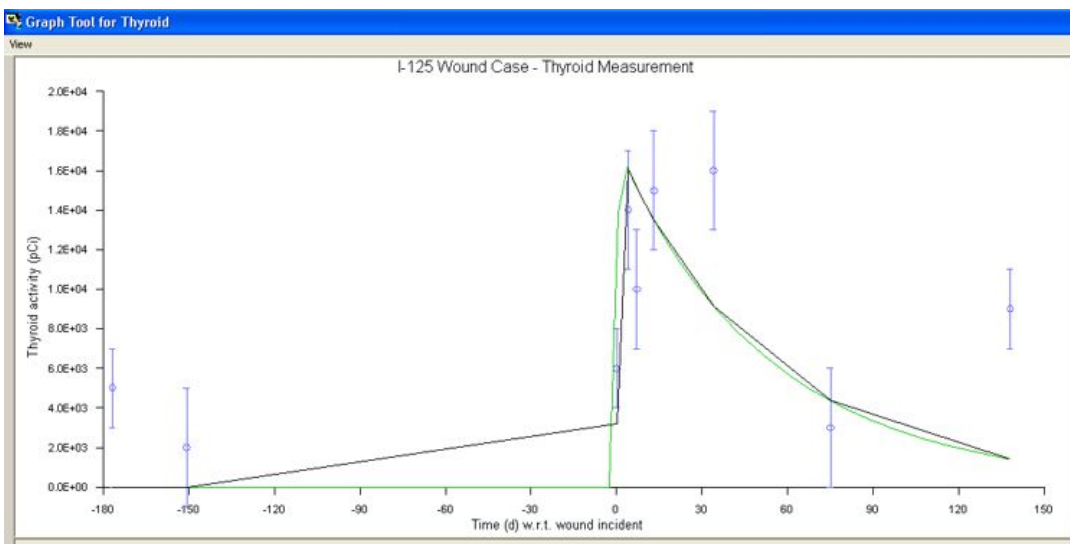


Figure D.152. Thyroid uptake and retention predicted for 'rapid' release of ^{125}I from the wound site to the blood.

The assumed uptake rate of 100 d^{-1} accounts well for the observed rapid initial uptake of ^{125}I by the thyroid, but not for the apparent “retention” of ^{125}I in the thyroid up to 34 d after the incident. The calculated total value of the χ^2 statistic (as shown in the Table Tool – Figure D.153) is **32.2**. This is substantially higher than the “expected” value (= 9), which is equal to the number of data points.

Measurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution	Theoretical Value(pCi)	Chi-Square
-1.769166667E+02		5.000E+03	Real	2.000E+03	NORM	0.000E+00	6.250E+00
-1.509166667E+02		2.000E+03	Real	3.000E+03	NORM	0.000E+00	4.444E-01
8.333333333E-02		6.000E+03	Real	2.000E+03	NORM	3.2291E+03	1.920E+00
4.083333333E+00		1.400E+04	Real	3.000E+03	NORM	1.6273E+04	5.741E-01
7.083333333E+00		1.000E+04	Real	3.000E+03	NORM	1.5341E+04	3.169E+00
1.308333333E+01		1.500E+04	Real	3.000E+03	NORM	1.3664E+04	1.984E-01
3.408333333E+01		1.600E+04	Real	3.000E+03	NORM	9.2471E+03	5.067E+00
7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	4.4183E+03	2.235E-01
1.380833333E+02		9.000E+03	Real	2.000E+03	NORM	1.434E+03	1.431E+01

Figure D.153. Calculated **Chi-Square** values for an assumed uptake rate of 100 d^{-1} .

However, as shown in Figure D.153, the first 2 data points (primarily the 1st point) contribute a large fraction of the total χ^2 , and these points are clearly NOT related to the incident (at time $t = 0$). Thus, the appropriate value of χ^2 to consider is that related to the 7 data points obtained “post-incident”. This value is **25.5**.

We can conclude that the assumption of an uptake rate of 100 d^{-1} from the wound site is NOT supported by the bioassay (thyroid) data. In the next section, we let **IMBA Expert™ OCAS/ORAU-Edition** itself “select” the most likely absorption behavior.

D.10.3. Deriving the Most Likely Absorption Rates

IMBA Expert™ OCAS/ORAU-Edition allows up to 10 intakes to be analyzed simultaneously. In this case, and many others for which critical **intake scenario** parameter values are UNKNOWN, this facility for simultaneous analysis provides a direct means of “fitting” the unknown parameter values. This is done by choosing an appropriately broad **range** of **hypothetical** values, and letting **IMBA Expert™ OCAS/ORAU-Edition** “rank” these values according to the **amount of intake** that it calculates for each. In this example, both the observed thyroid “retention” and the measured retention of contamination on the worker’s hand suggest that a significant component of the absorption occurs **slowly**.

In this example, in order to examine the degree of “slow uptake”, we have set up 6 simultaneous acute ‘wound’ intakes at time $t = 0$. The ‘hypothetical’ rates tested are:

- IR1 = 100 d^{-1} ;
- IR2 = 0.2 d^{-1} ;
- IR3 = 0.1 d^{-1} ;
- IR4 = 0.05 d^{-1} ;
- IR5 = 0.02 d^{-1} ;
- IR6 = 0.01 d^{-1} .

Figure D.154. shows the resulting amounts of intake calculated using the maximum likelihood method for each of these 6 hypothetical intake scenarios, and the resulting overall ‘fit’ to the

observed thyroid retention. The corresponding calculated values of χ^2 are shown in Figure D.155 (as displayed in the **Table Tool**).

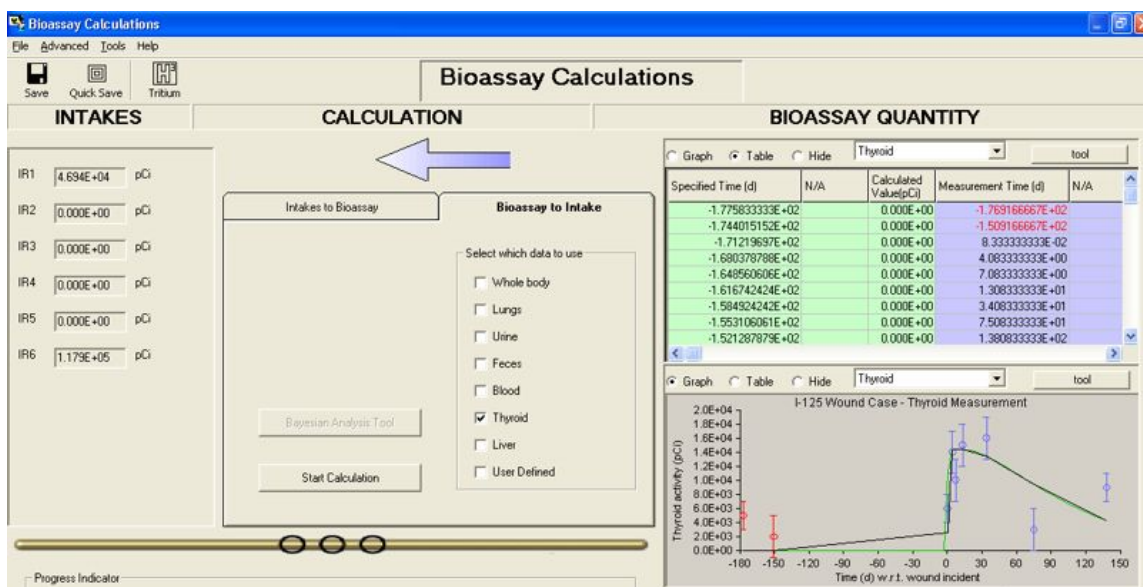


Figure D.154. Data 'fit' obtained with 6 hypothetical absorption rates.

Measurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution	Theoretical Value(pCi)	Chi-Square
-1.769166667E+02		5.000E+03	Excluded	2.000E+03	NORM	0.000E+00	0.000E+00
-1.509166667E+02		2.000E+03	Excluded	3.000E+03	NORM	0.000E+00	0.000E+00
8.333333333E-02		6.000E+03	Real	2.000E+03	NORM	2.586E+03	2.914E+00
4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM	1.4230E+04	5.866E-03
7.083333333E+00		1.0000E+04	Real	3.000E+03	NORM	1.4330E+04	2.083E+00
1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM	1.4375E+04	4.339E-02
3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM	1.3368E+04	7.698E-01
7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	9.3907E+03	4.538E+00
1.380833333E+02		9.000E+03	Real	2.000E+03	NORM	4.2767E+03	5.577E+00

Figure D.155. Calculated values of χ^2 for 6 hypothetical absorption rates.

The calculated intake amounts are:

- IR1 = 46,940 pCi;
- IR2 = 0 pCi;
- IR3 = 0 pCi;
- IR4 = 0 pCi;
- IR5 = 0 pCi;
- IR6 = 117,900 pCi.

In other words, **IMBA Expert™ OCAS/ORAU-Edition** calculated a total intake of 164,840 pCi, with 28.5% of this assigned an absorption rate of 100 d⁻¹ and 71.5% the slowest assumed absorption rate of 0.01 d⁻¹. The total χ^2 is now reduced to **17.1**. This is significantly lower than the previous value (obtained for 100% absorption at a rate of 100 d⁻¹), but it is still significantly higher than the "expected" value (for the 7 residual data points).

However, the largest χ^2 contribution (of 5.6) is made by the data point obtained at 138 d after the incident. We can examine the effect of treating this point as an “outlier” by marking it as “**excluded**” in the **Table Tool** (as we did for the first 2 data points – prior to the incident). The effect of excluding the last data point from the ‘fit’ is shown in Figure D.156.

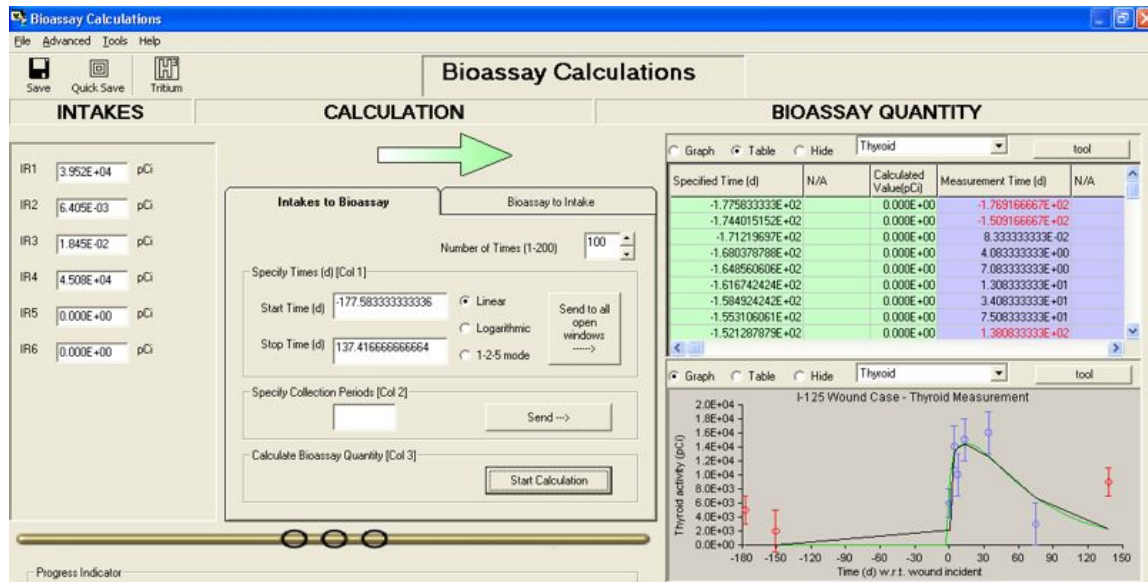


Figure D.156. Data ‘fit’ obtained by excluding the data point at 138 d.

Treating the data point at 138 d as an “outlier” clearly improved the ‘fit’ of predicted thyroid retention of ^{125}I to the remaining 6 measured values. The resulting values of χ^2 are shown in Figure D.157 (from the **Table Tool**).

Measurement Time (d)	N/A	Measurement Value(pCi)	Data Type	Measurement Error	Error Distribution	Theoretical Value(pCi)	Chi-Square
-1.769166667E+02		5.000E+03	Excluded	2.000E+03	NORM	0.000E+00	0.000E+00
-1.509166667E+02		2.000E+03	Excluded	3.000E+03	NORM	0.000E+00	0.000E+00
8.333333333E-02		6.000E+03	Real	2.000E+03	NORM	2.1808E+03	3.647E+00
4.083333333E+00		1.4000E+04	Real	3.000E+03	NORM	1.3114E+04	8.730E-02
7.083333333E+00		1.0000E+04	Real	3.000E+03	NORM	1.3784E+04	1.591E+00
1.308333333E+01		1.5000E+04	Real	3.000E+03	NORM	1.4369E+04	4.419E-02
3.408333333E+01		1.6000E+04	Real	3.000E+03	NORM	1.2555E+04	1.319E+00
7.508333333E+01		3.000E+03	Real	3.000E+03	NORM	6.7252E+03	1.542E+00
1.380833333E+02		9.000E+03	Excluded	2.000E+03	NORM	2.2242E+03	0.000E+00

Figure D.157. Calculated values of χ^2 after excluding the data point at 138 d.

The total χ^2 is now reduced to **8.2**, which is a substantially more likely value (for 6 residual data points).

Notice also (from Figure D.156) that the intake amounts assigned to each of the 6 hypothetical absorption rates have now changed substantially. The new values are:

- IR1 = 39,520 pCi;
- IR2 = 0.0064 pCi;
- IR3 = 0.018 pCi;

- IR4 = 45,080 pCi;
- IR5 = 0 pCi;
- IR6 = 0 pCi.

In other words, neglecting both IR2 and IR3, **IMBA Expert™ OCAS/ORAU-Edition** calculated a significantly smaller total intake of 84,600 pCi, with 46.7% of this assigned an absorption rate of 100 d^{-1} and 53.3% assigned an absorption rate of 0.05 d^{-1} . The corresponding 'retention function' is:

$$R_{\text{thyroid}}(t) = 0.467 \exp(-100t) + 0.533 \exp(-0.05t) \dots\dots\dots (D.1).$$

This function can now be entered directly in the '**Generic Wound Model**' window to define the most likely absorption behavior for the single acute intake in this case (Figure D.158).

The screenshot shows a software window titled 'Generic Wound Model'. At the top, it displays the retention function formula: $Ret(t) = a(1) \exp[-\lambda(1)t] + a(2) \exp[-\lambda(2)t] + \dots$. Below this, there are two main sections. On the left, under 'Select', there is a 'User Defined Mode' button and a group box 'NCRP Defaults' containing four buttons: 'Weak', 'Moderate', 'Strong', and 'Avid'. At the bottom left is a 'User Defined' label. On the right, under 'Wound Retention', there is a table with 5 rows and 2 columns: 'i', 'a(i)', and 'lam(i)'. The first two rows are populated with values: (1, 0.467, 100) and (2, 0.533, 0.05). Below the table is a 'Clear' button. At the bottom of the window are 'OK' and 'Cancel' buttons.

i	a(i)	lam(i)
1	0.467	100
2	0.533	0.05
3		
4		
5		

Figure D.158. Derived absorption behavior of ^{125}I needle-puncture wound.

In the next section, we use the integrated Bayesian Analysis 'tool' to calculate the posterior probability distribution of intake for this case.

D.10.4. Calculating the Posterior Probability Distribution of Intake

Having entered the derived retention function [in the form of Equation (D.1)], we can now use **Bayesian Inference** to calculate the posterior probability distribution of intake and its associated statistics. This is done in the **Bioassay Calculations** screen, by first selecting the '**Bayesian**' radio button from the **Advance | Fitting Options | Fitting** menu. Clicking the 'Start Calculation' button then gives the result (calculated intake amount and resulting data 'fit') shown in Figure D.159. As expected, the calculated (mean) intake value (85,220 pCi) is close to the total intake value obtained earlier (84,600 pCi) using the **maximum likelihood method** (with non-rounded parameter values). The resulting 'fit' to the bioassay data is shown in Figure D.160.

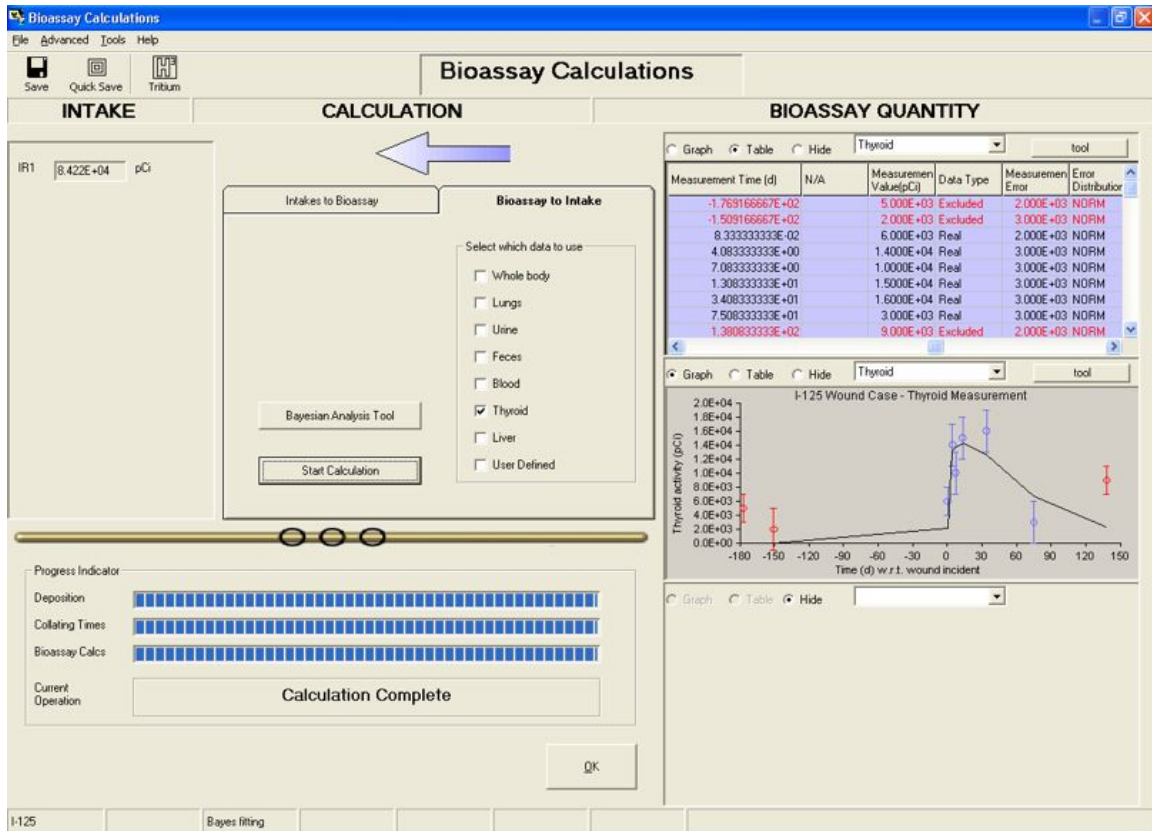


Figure D.159. Calculated mean value of the intake distribution using the 'Bayesian' fitting option.

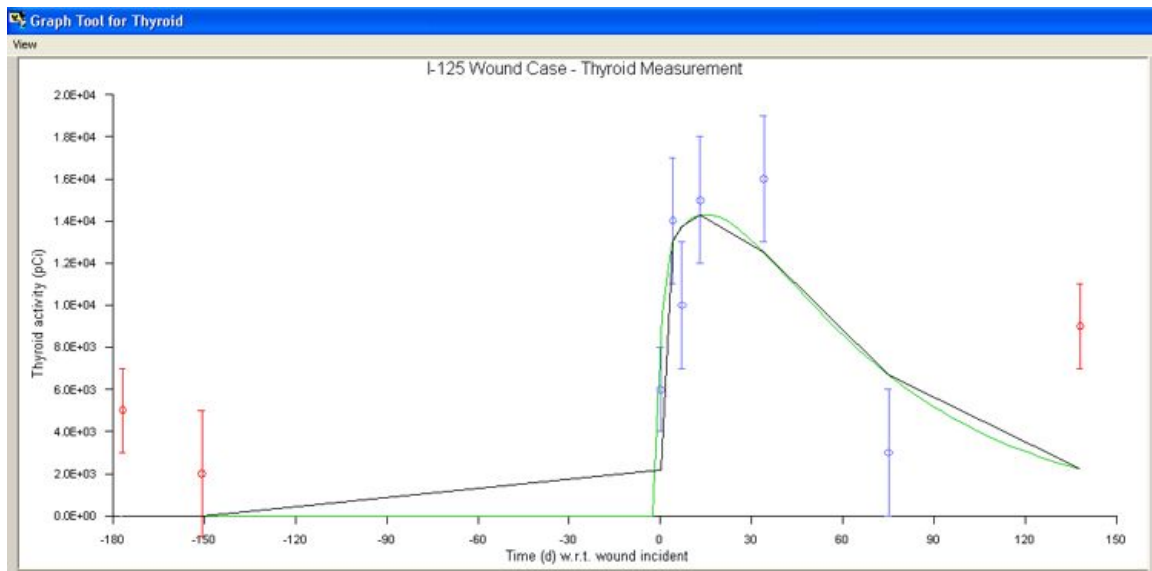


Figure D.160. Dat 'fit' obtained with derived wound retention function.

In the 'Bayesian Analysis Tool' (Figure D.161), we will select a 'Uniform' prior probability distribution of intake, over the range 1 pCi to 1,000,000 pCi (1 μ Ci).

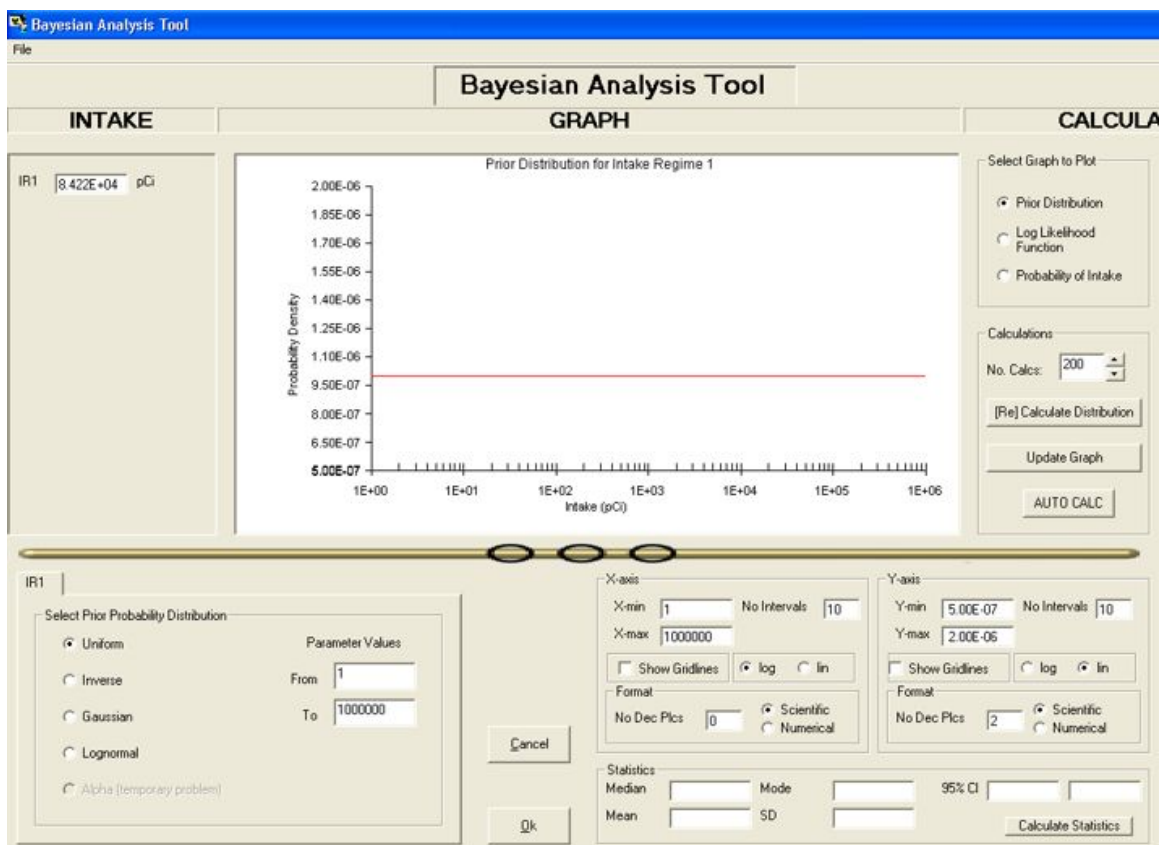


Figure D.161. Selecting a 'Uniform' prior in the 'Bayesian Analysis Tool'.

The calculated 'Log-Likelihood Function' is shown in Figure D.162.

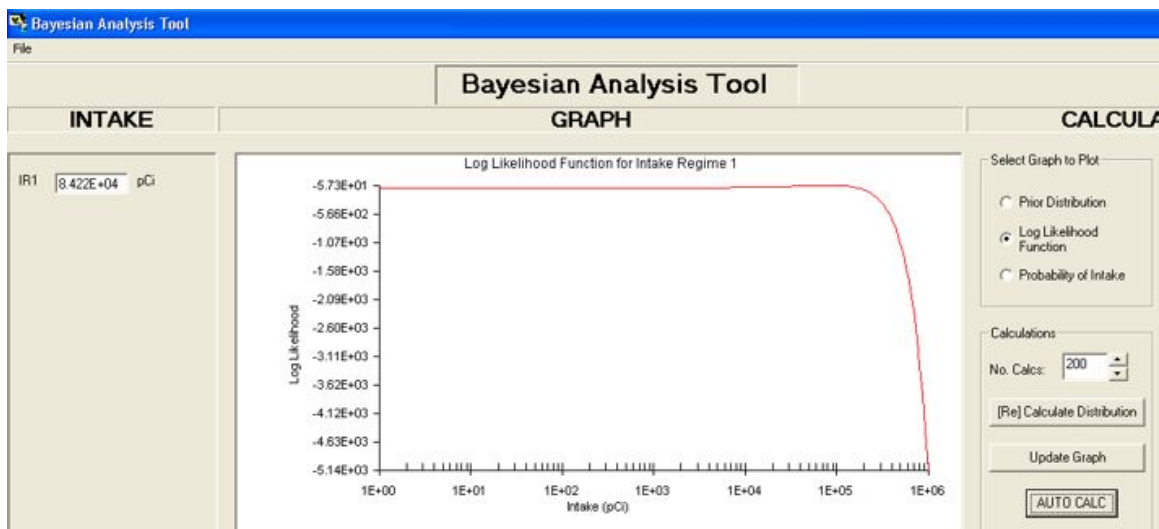


Figure D.162. Calculated Log-Likelihood intake distribution for ^{125}I wound case (with 'Uniform' prior).

The resulting calculated 'posterior' probability distribution for the intake amount is shown in Figure D.163.

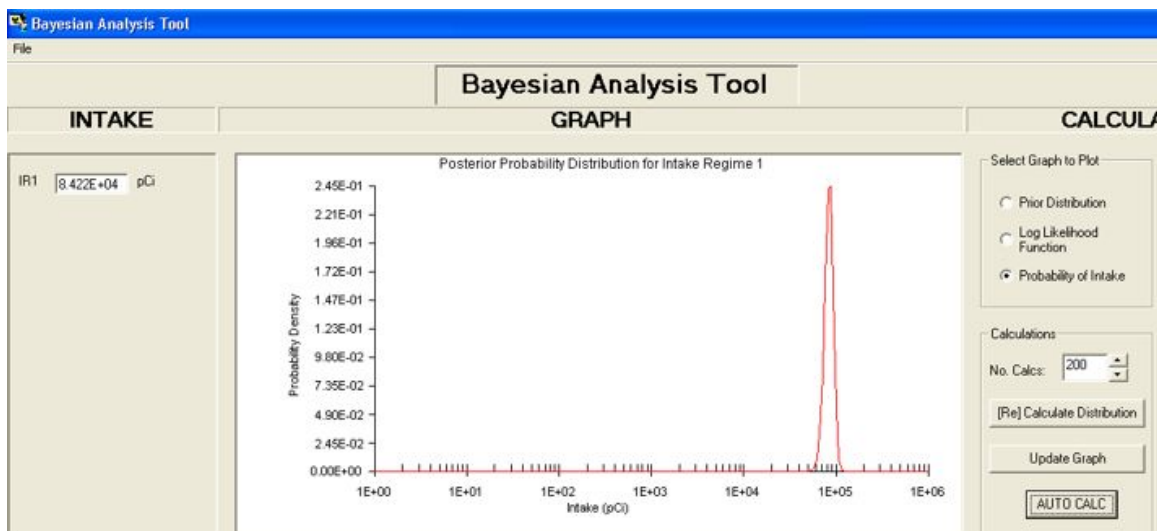


Figure D.163. Calculated posterior probability distribution for the amount of intake.

The calculated 'statistics' of the posterior probability distribution are shown in Figure D.164.

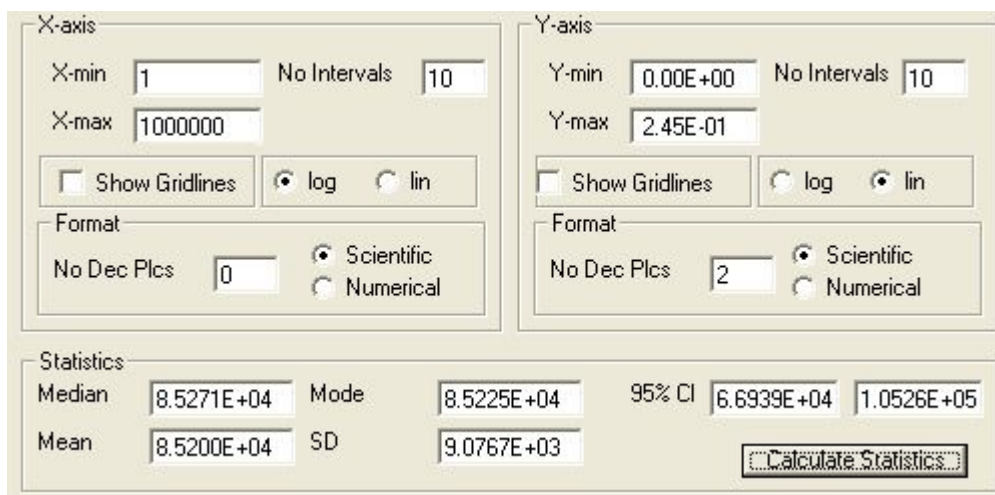


Figure D.164. Calculated 'statistics' of the posterior probability distribution.

The calculated 'statistics' of the posterior probability distribution of intake amount are:

- **Median** value = 85,271 pCi;
- **Modal** (most likely) value = 85,225 pCi;
- **Mean** value = 85,200 pCi;
- **Standard Deviation** = 9,077 pCi, *i.e.*, 10.7% of the **Mean**;
- **95% Confidence Interval** = 66,939 pCi – 105,260 pCi.

D.11. References

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³ http://www.deploymentslink.osd.mil/du_library/lab_assessment/lab_assessment_refs/n72en010/2193_018_0000032.htm.